

Population variation in characteristic aspects of children's behavior and frequency of child behavior problems: Colombian and US samples. A.A. BREWIS and R.W. KAMPHAUS, Departments of Anthropology (AAB) and Educational Psychology (RWK), The University of Georgia, Athens, GA 30602.

Biological anthropology is concerned fundamentally with human variation, including in behavior. Schizophrenia research has demonstrated the utility of this approach to advance understanding of psychiatric disorders, both in terms of variation in symptomatic expression between groups and in definitions of behavioral (ab)normality in diagnosis. In comparing characteristic behavior patterns of children in classrooms in Colombia to a National US sample using an identical tool, this study explores the utility of such an approach for understanding the 'epidemic' of child behavioral and learning problems that has emerged within the US and - more recently - in international contexts.

The tool used to compare child behavior patterns in these two populations measures the frequency of child behavior problems and characteristic aspects of child's behavior as perceived by teachers (Reynolds and Kamphaus 1992, *Behavior Assessment System for Children*). The scales cover 14 aspects of behavior: aggression, anxiety, attention (+ve), atypicality, conduct problems, depression, hyperactivity, leadership (+ve), learning problems, social skills (+ve), social adaptability (+ve), somatization, study skills (+ve), and withdrawal.

Colombian data were collected in Medellin in 1997-98. The sample of 330 is intended to be representative of local population of the metropolitan area. The US data ($N=1226$) represent a stratified nationally representative sample of the US population taken in 1989-90. Both samples contain an even age and sex distribution of children aged 6-11 years. The population differences in distributions for each behavioral feature were compared by one way ANOVA. All analyses were done with both sexes combined, as is standard practice in child psychological studies employing this tool.

These data demonstrate significant population variation in frequency distributions of some features of (ab)normal child behavior ($P<0.01$), such as in attention and hyperactivity. By contrast, the distribution of other aspects of typical child behavior appears more robust ($P>0.01$), such as anxious, depressive, and aggressive symptoms. In demonstrating population variation in distribution of some but not all identified 'problem' symptoms, this approach promises improved understanding of the cross-population utility of diagnostic criteria of such child behavioral conditions as Attention Deficit Hyperactivity Disorder among others.

Approaches to the study of Osteoporosis: Key findings from a comparative study. M.B. BRICKLEY. Department of Ancient History and Archaeology, The University of Birmingham, Birmingham B15 2TT, United Kingdom.

This paper is the result of an extensive study, in which eleven techniques used to investigate osteoporosis in archaeological bone were compared on a sample of London skeletal material.

Osteoporosis is a metabolic disease of bone. Throughout life bone is continually being remodelled. In a normal, younger, healthy individual bone formation and resorption are balanced. However, with age and some medical conditions the two sides of this

process may no longer be in equilibrium, leading to a net loss of bone (osteopenia). In extreme cases, (osteoporosis), this can lead to fractures occurring.

The condition is now regarded as a major health problem in many areas of the world, due to the huge personal and financial cost caused by osteoporosis related fractures.

A growing awareness of the condition, and the morbidity and mortality that can result from fractures, has led a number of researchers to investigate the past prevalence of the condition. To date a wide variety of techniques have been employed to study the condition.

The key points relating to some of the techniques used in the present study are outlined. Investigative techniques included are; visual examination, dual energy x-ray absorptiometry, energy dispersive low angle x-ray scattering, close range photogrammetry, optical densitometry, the Singh Index and measure of cortical thickness.

As researchers work in a variety of situations no one technique is advocated. Rather the advantages and disadvantages of a range of techniques are summarised, taking into consideration factors such as the possibility of obtaining misleading results due to diagenesis, availability of equipment, and the time and cost involved in using techniques.

Biomechanics of long bone diaphyses from Cochiti Reservoir, New Mexico. P.S. BRIDGES, Anthropology, Queens College and CUNY Graduate Center, Flushing, NY 11367, M.O. SMITH, Anthropology, Northern Illinois University, Dekalb, Illinois, 60115, and M.C. SOLANO, Anthropology, University at Albany, SUNY, Albany, NY 12222.

The Cochiti Dam Salvage Archaeological Project resulted in the excavation in the 1960s of five sites with human osteological remains. Two late prehistoric sites yielded relatively large numbers of individuals: Encierro (LA70, $N=116$) and Alfred Herrera (LA6455, $N=86$). A subset of these remains was complete enough for biomechanical analysis.

A computed tomographic scanner was used to derive cross-sections of humeral and femoral diaphyses. These sections were digitized, yielding estimates of cortical area, minimum and maximum bending strengths, and torsional strength.

When compared to a range of hunter-gatherer, horticultural, and agricultural groups from the Eastern Woodlands of Alabama and Illinois, Cochiti males and females had lower femoral strength than any of the other samples. However, humeral strength at Cochiti was largely within the range for the Eastern groups. Female humeral strength on the right side alone slightly exceeded the highest value for females of the Eastern Woodlands.

These data add to our information on the diversity of agricultural adaptations in prehistoric North

America. They suggest that some southwestern groups may have been less mobile than societies of the Eastern Woodlands. However, arm strength, especially of females, is relatively high, possibly as a result of their participation in agricultural or processing chores.

Supported in part by the U.S. Army Corps of Engineers.

The brain-face interface: Does brain size correlate with facial dimensions in *Homo* and *Pan*?

D. BROADFIELD^{1,2}, K. MOWBRAY¹, S. MARQUEZ^{1,2}, J.T. LAITMAN^{1,2}, and R.L. HOLLOWAY², Department of Cell Biology and Anatomy, Mount Sinai School of Medicine¹, NY, NY 10029, Department of Anthropology, City University of New York², NY, NY 10036, Columbia University³, NY, NY 10027, Rutgers University⁴, New Brunswick, NJ 08903

The relationship of the size and morphology of the brain to the architecture of the facial skeleton has long been of interest. Current research, however, has not demonstrated a correlation between facial dimensions and brain size. For example, Conroy et al. (1998) and Falk (1998) have suggested a cranial capacity for *Sts 71* which is lower than a comparably sized South African specimen (*Sts 5*), albeit they share similar facial dimensions. We expect brain growth to have some influence on certain cranio-facial dimensions, but to what degree endocranial capacity correlates to facial dimensions has yet to be determined. This study explores this relationship using traditional morphometrics on three geographically distinct human groups and a natural population of Liberian chimpanzees (*Pan troglodytes*).

Human and chimpanzee adult crania were selected from the Peabody Museum, Harvard University, the Hamon-Todd Collection, Cleveland Museum of Natural History, and the Department of Anthropology at the American Museum of Natural History. Cranial specimens reflect an extant mixed sex sample of regional populations including Egyptians (n=38), South Africans (n = 11), and Northern Europeans (n = 41), and as an added comparator the inclusion of *Pan* (n = 35). A total of 18 standard craniometric measurements (e.g., orbital width, facial height) were taken on each skull. These measurements were then correlated to brain size, which was calculated through graduated volumetric measurements by seed filling.

Results show a correlation between certain facial dimensions (e.g., facial height, orbital height) and cranial capacity with regard to within taxon comparisons for both *Pan* and *Homo*. Correlation coefficients range from $r = 0.36$ ($p \leq 0.02$) to $r = 0.62$ ($p \leq 0.0001$). This suggests that cranial capacities for individuals within a taxon should be similar if certain facial dimensions are also similar. The consistency of such results in *Homo* and *Pan* further suggest that such measures may be of value in deriving cranial capacity in fossil hominids. This research is supported under NSF grant SBR9528100.

Group transfer and male competition in *Propithecus verreauxi*: Insights into factors mediating male infanticide in a seasonally breeding primate. D.K. BROCKMAN¹ and P.L. WHITTEN.² ¹Department of Biological Anthropology and Anatomy, Duke University, Durham, NC 27708, ²Departments of Anthropology and Biology, Emory University, Atlanta, GA 30322.

Ecological and social environments mediate the degree of testicular seasonality in mammals, but little is known regarding how these factors interact in a "strictly" seasonal primate like *sifaka*. Previous pilot investigations of *Propithecus verreauxi* (Brockman et al., 1998) suggest that elevated fecal testosterone levels may be associated with male aggression and group instability during the birth season, infanticide potentially occurring in conjunction with increased aggression during immigration. Here we report the results of a nine-week study of androgen-behavior relationships associated with group transfer and aggressive competition in male *P. verreauxi* at Beza Mahafaly, Madagascar.

Weekly censuses conducted during the June-August 1998 birth season showed that 60% of 30 social groups were unstable, undergoing a change in male membership just prior to and during the birth season. Results of behavioral and hormonal data collected on 17 males in 6 unstable focal groups showed that males were most successful immigrating into groups without infants. Age-specific differences occurred in levels of aggression during transfer, younger males moving more often and incurring substantially less aggression than older males. Older males voluntarily emigrated, were evicted from groups via targeted aggression, or were recruited during female takeovers. Older males attempting to immigrate into groups containing newborns were avoided by mothers and successfully repulsed by resident males, supporting recent demographic data (Richard et al., in prep) suggesting that male infanticide might be selected for only weakly in this population. Supported by grants from the Margot Marsh Biodiversity Foundation and ASRC of Duke University.

Ethnic difference in the relationship between ambulatory blood pressure and age in school teachers in Hawaii: Japanese-Americans and Caucasians. D. E. BROWN, S. L. AKI, M. B. ETRATA, A. A. JONES, Anthropology, University of Hawaii at Hilo, Hilo, HI 96720, and G. D. JAMES, Nursing, Binghamton University, NY 13902.

Japanese-Americans (JAs) in Hawaii have high rates of hypertension and stroke compared with

state and Caucasian (C) averages. Accordingly, ambulatory blood pressure (BP) measurements were recorded of 97 female teachers of JA (N=66) or C (N=31) ethnicity working in public schools located in Hilo, Hawaii. BP was measured at 15 min intervals during waking hours and 30 min intervals during sleep over a 24 hr period that included a full work day. These measurements were averaged during three daily settings: at work, at home while awake ('home'), and during sleep. There were no significant ethnic differences in mean BP in any of the daily settings (t-tests).

Correlations between age and BP were carried out separately for the two ethnic groups. Among JAs, correlations between age and systolic BP are significant at work ($r=0.46$), home ($r=0.44$) and during sleep ($r=0.41$, $p < 0.001$ in all settings); among Cs the correlation is only significant in the work setting (work: $r=0.40$, $p < 0.05$; home: $r=0.31$, ns; sleep: $r=0.25$, ns). For correlations between age and diastolic BP, for JAs correlations are significant in all settings (work: $r=0.38$; home: $r=0.33$; sleep: $r=0.45$; $p < 0.01$ for all settings), while among Cs these correlations are not significant in all settings (work: $r=0.26$; home: $r=0.21$; sleep: $r=0.23$). This greater increase in BP with age in JAs may be related to their elevated risk for development of hypertension.

Supported by NIH-MBRS Grant No. SO6-GM/HL 08073-27 and by a grant from the American Heart Association - Hawaii Affiliate.

Evidence of stress and variation within the Fort Ancient Culture of the Ohio River Valley. E. A. BROWN, A.L. GRAUER, Department of Sociology and Anthropology, Loyola University of Chicago, Chicago, IL 60626, and E.M. MCNAMARA, Department of Anthropology, University of Illinois, Urbana, IL 61801.

The Fort Ancient Culture, occupying a large portion of the Ohio River Valley from A.D. 950-1670, is characterized by maize and bean agriculture. Skeletal analyses of populations associated with this culture have reported high frequencies of enamel hypoplasias, porotic hyperostosis, periosteal reaction and caries. Variation, however, in frequency rates of pathologies has been found between populations. This paper demographically and paleopathologically examines a skeletal population ($n=52$) excavated by Warren Moorehead in 1891-92. Comparisons are made to other skeletal analyses in an effort to explore how and why this archaeologically constructed culture varied.

The results of the demographic examination indicate that 48% (25/52) of the skeletal sample were below the age of 15. Enamel hypoplasias are found

on 48% (12/25) of the total population exhibiting permanent canines. Caries are present on 31% (11/36) of the individuals with a permanent molar. 76% (31/41) of the population display porotic hyperostosis, and 94% (49/52) of population display periosteal reaction.

It appears that this population was experiencing substantial levels of stress. Comparisons to other populations associated with the Fort Ancient Culture provide insights into the extent and potential sources of this stress.

This research has been supported by NSF Grant No. SBR-9350256.

Early behavioral development in a wild white-faced saki monkey (*Pithecia pithecia*). J.A. BRUSH and M.A. NORCONK, Anthropology, Kent State University, Kent, OH 44242.

While developmental data on the white-faced saki (*Pithecia pithecia*) is growing, information from the wild has been scarce. This paper contributes the first study of the early development of the wild white-faced saki using three major behavioral categories. Early ontogenetic patterns in nursing and sleeping time as well as locomotor skills were tracked for an infant in Lago Guri, Venezuela. The infant matured from approximately 5 to 12 weeks of age over the eight-week middle-dry season study (Jan/Feb 1998).

The frequency and duration of nursing and sleeping activities contributed less to this sample of the infant's behavioral repertoire than behaviors related to increasing locomotor independence (e.g. quantity of time off and distance from the mother, etc.). Both daytime sleeping and nursing were rare activities ("naps" $n = 4$ obs; nurse $n = 20$) with most nursing relegated to morning wake-up and afternoon retiring periods (75%; total nursing sample: 3285s).

Ontogenetic trends in locomotor independence were demonstrated in mean distance from the mother. The beginnings of independence were observed with mean distances ranging between <1m to 2m in weeks 5-8. Values peaked at over 10m in weeks 9-12 which coincided with the beginning of infant "parking." "Parking" began late in week 9 in both terrestrial and arboreal contexts.

Carrying by other group members appeared to be initiated by infant separation calls and to be correlated with infant "parking." No other group members contributed to infant carrying until the infant's 12th week. Alternative carriers consisted only of the eldest female sibling and the subadult male sibling with the latter being the principle carrier (non-maternal carrier time sample = 648s; 5% by "sister", 95% by "brother").

These preliminary findings on the locomotor and behavioral ontogeny of *Pithecia* are intermediate between the more altricial pattern for *Cebus* and the very precocial pattern for *Saimiri* and certain old world monkeys. Data on wild sakis indicate that variation with respect to "maternal style" is in need of exploration to better understand *Pithecia*'s behavioral development.

Patterns of craniometric sexual dimorphism in papionin primates. L.S. BUCHANAN and S.R. LEIGH. Department of Anthropology, University of Illinois, Urbana.

Variability in patterns of sexual dimorphism in skeletal morphology has important implications for inferences about behavior, ecology, and evolution in extant and fossil species. We analyze patterns of craniometric dimorphism in extant papionins in order to determine the degree of uniformity in sexual dimorphism among taxa. Papionins exhibit a range of variation in the degree of size dimorphism, but our understanding of the pattern of dimorphism remains limited.

We analyze linear dimensions from eleven papionin species. Measures representing the face, neurocranium, and basicranium are evaluated in order to provide information about overall patterns of cranial dimorphism. These data are subjected to Andrews' Fourier plot analyses, following protocols established by Oxnard (1983; *Am. J. Primatol.*).

The degree of size dimorphism varies among these taxa, ranging from very high levels in mandrills to moderate levels in mangabeys. The degree of dimorphism also varies among cranial components. Patterns of sexual dimorphism in papionins appear to be quite conservative. Fourier plots of linear data generally show consistent profiles of multivariate similarities both within and among species. Analyses of shape data also suggest similar patterns of shape dimorphism.

These results suggest the presence of consistent patterns of sexual dimorphism in papionins, despite considerable variation in the degree of size dimorphism. The consistency of these patterns may imply either common underlying responses to sexual selection or the existence of functional and developmental constraints on the cranium. The implications of these results for analyses of morphological integration and for interpretation of fossil materials are discussed.

This research was supported by NSF (SBR 9707361), Wenner-Gren, the Leakey Foundation, and the University of Illinois.

Spatial distribution of coronal sutural bones in familial coronal suture synostosis. A.M. BURROWS, M.J. FABRIZZI, T.D. SMITH, Slippery Rock University, Slippery Rock, PA 16057, M.P. MOONEY, H.W. LOSKEN, M.I. SIEGEL, University of Pittsburgh, Pittsburgh, PA 15260.

Previous studies using a rabbit model of familial delayed onset coronal suture synostosis have revealed that affected crania have significantly more coronal sutural bones than normal crania. Synostosis in this rabbit model begins in the intermediate region of the coronal suture and expands to the lateral and medial regions. If ectopic bone formation in the coronal suture is a precursor to premature sutural fusion, then more sutural bones will occur in the intermediate region of the coronal suture than in the lateral and medial regions. This hypothesis was tested using crania from 21 adult New Zealand white rabbits with delayed onset coronal

suture synostosis and at least one coronal sutural bone. Coronal sutures were divided into lateral, intermediate, and medial regions and sutural bones were counted in each suture region. Results of chi-square analysis showed that rabbits with delayed onset coronal suture synostosis had significantly ($p < 0.05$) more sutural bones in the medial and intermediate regions of the coronal suture than in the lateral region, and that there were significantly more sutural bones in the medial region than in the intermediate region. These results reflect those from previous studies of this rabbit model, which have shown the medial region of the coronal suture to be undergoing a high amount of compensatory growth and deformation. In addition, these results suggest that biomechanical factors may be more influential than genetic factors in sutural bone formation.

Supported in part by NIDR (DE10830), Plastic Surgery Education Foundation, and Central Research Development Fund, University of Pittsburgh.

Comparison of paraseptal (vomeronasal) cartilages in adult humans and mouse lemurs. T.A. Buttery, T.D. Smith, A.M. Burrows, School of Physical Therapy, Slippery Rock University, Slippery Rock, PA 16057, M.P. Mooney, M.I. Siegel, Department of Anthropology, University of Pittsburgh, Pittsburgh, PA 15260.

In the past, conflicting evidence has been presented regarding the existence of paraseptal (vomeronasal) cartilages (PCs) in humans. With this controversy, previous research has done little to examine PCs in humans and even less attention has been paid to the comparison of human PCs with those of other primates.

Histologically sectioned nasal septa from 15 adult human and three adult mouse lemur (*Microcebus murinus*) cadavers were examined for the presence of PCs. Lengths were obtained based on serial sections and percent of palatal length (PCPL) was calculated (PC length/palatal length).

Paraseptal cartilages were found in all human and lemur specimens. The morphology of PCs was found to have some similarities between humans and lemurs. Lemur specimens contained nasal and palatine processes of the PC in anterior sections. These processes joined to form a unified PC as the nasal process rotated downward to join the palatine process. This relationship was also seen in human PCs, but there were a greater number of separate cartilage processes seen in anterior sections for humans. In humans, PCs began as distinct lobes of hyaline cartilage lying lateral to the inferior tip of the nasal septum. Progressing posteriorly, PCs became gracile and extended appendages in a superolateral direction. The appendages rotated downward until they assumed a position that extended below the nasal septum at their posterior-most extent. Quantitative measures showed that mean PC length was 1.55cm in humans and 0.68cm in lemurs. PCPL was approximately 31% in humans and 37% in lemurs. Although absolute PC size differences were found to exist, the proportional size relative to palatal length was more similar. The presence of PCs in humans remains clear.

Supported in part, by a grant from the College of Health and Human Services, Slippery Rock University.

Environmental change, sociopolitical power and the diet and health of elites during the emergence of the Tarascan state. L. CAHUE, Department of Anthropology, Michigan State University, East Lansing, MI 48824.

This paper examines the extent to which the interaction of environmental change and sociopolitical power affected the diet and health of elite populations in the Lake Patzcuaro basin during the formation of the Tarascan state. The Tarascan state emerged during the Postclassic (A.D. 900 - A.D. 1500) in the Lake Patzcuaro basin. Data from sediment cores from Lake Patzcuaro (O'Hara et al., 1993) indicate that lake water levels fluctuated during this time. These lake level fluctuations resulted in shifts in food production potential. Food production potential, population estimates and consumption needs for the Lake Patzcuaro basin indicate that, by the Late Postclassic, the basin was unable to produce enough food for its population (Pollard, 1993). How did the Tarascan empire, the second largest in Mesoamerica and one that dominated western Mexico at the time of European contact, thrive under such dietary constraints?

Ethnohistoric evidence indicates that maize was a major tribute item flowing into the basin. Using this evidence, Pollard (1993) proposed that the pattern of warfare established prior to the political unification of the basin was later used to secure foodstuffs from throughout the Empire. This implies that an emergent, socially stratified elite class in the Lake Patzcuaro basin would have had the sociopolitical and economic power to obtain maize from outside the basin, protecting the elite against dietary change and the potential stress of calorie-energy malnutrition. To test this hypothesis, stable carbon and nitrogen isotope values ($\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values respectively) of bone collagen will be used to assess temporal variation in the diet of elites. Skeletal and dental indicators of nutritional deficiencies and infectious diseases will be discussed in relation to diet. Since this is the first bioarchaeological study of the impact of state formation, and the conditions under which it took place, on the health and nutrition of human populations in the region, it makes a valuable contribution to our understanding of Mesoamerican prehistory.

Reinvestigating the number of hominid species in Sterkfontein Member 4. J.M. CALCAGNO, Loyola University of Chicago, Chicago, IL 60626, D.A. COPE, College of Charleston, Charleston, SC 29424, M.G. LACY, Colorado State University, Fort Collins, CO 80523, J. MOGGI-CECCHI and P.V. TOBIAS, University of the Witwatersrand, Johannesburg, South Africa.

In a previous investigation into whether *A. africanus* is the only hominid species represented in Member 4 of Sterkfontein (based on STW remains), Calcagno et al. (1997) suggested that a multiple-species interpretation best fit their odontometric data and therefore merited further examination. In 1998, Lockwood and Moggi-Cecchi supported this claim with detailed morphological studies of particular specimens

(STW-183; STW-151). Member 4 has been rich in hominid fossils, and commonly all were previously assigned to *A. africanus*.

In the current study, material labelled STW and STS (the latter including specimens discovered before 1966) is examined, thus greatly increasing sample sizes relative to the 1997 analysis (from N=4-19 to N=20-34). To investigate whether the Member 4 hominids represent only one species, variability in posterior dental characters was tested using the Combined CV method of Cope and Lacy (1995), in which the CV for a fossil sample dimension is compared to a weighted average of CVs from a set of reference samples. The current analysis used two different referent sets, one comprised of our closest living non-human primate relatives (chimps, bonobos, and gorillas), and a second which contains more dimorphic species for a more conservative test of the single-species null hypothesis. A supplementary analysis applied a version of Levene's test (Schultz, 1985), using a gorilla and chimp sample for comparison.

Among the eight dental dimensions examined, the CV analysis indicated statistically significant elevated variation for only two (Max M2 Lt and Br), and Levene's test indicated one dimension (Max M2 Br) as excessively variable. Thus, we cannot recommend rejection of a single-species hypothesis on this basis alone, although both approaches suggested a statistically non-significant pattern of elevated variation. These results, in the context of recent morphological studies, highlight the difficulties in applications of purely statistical approaches to detecting multiple species in some fossil samples.

Stunting and nutritional intake from birth to five years in urban African children from Soweto, South Africa. N. CAMERON, Department of Human Sciences, Loughborough University, UK and Department of Anatomical Sciences, University of the Witwatersrand Medical School, Johannesburg, South Africa. and JM MCKEOWN, Dental Research Institute, University of the Witwatersrand Dental School, Johannesburg, South Africa.

Stunting defined as an NCHS height Z-score less than -2, is generally accepted as a *permanent* consequence of poor nutrition during infancy. Previous analyses of growth data from Soweto, South Africa confirmed a high prevalence of stunting at 2 years of age (19%) but also identified a general increase in growth status (height and weight) and a reduced prevalence of stunting between 4 and 5 years of age (5%). Stunted children appeared to demonstrate "catch-up" growth between 2 and 4 years with highly significant negative correlations between degree of stunting at 2 years and height increment from 2 to 4 years. The present analysis sought to determine the pattern of nutritional intake in the stunted and non-stunted children with the aim of explaining catch-up growth through differential quality/quantity of food intake.

The Birth To Ten birth cohort study (BTT), of singleton births that occurred in the Soweto-Johannesburg metropolis between April 23rd and June 8th 1990, provided a sample of 644 African children of normal gestational age (36-40 weeks) of whom 147 (22.8%) were stunted at 2 years of age. Nutritional intake was determined through food frequency

questionnaires carried out by trained field workers at 12 months and 5 years.

Whilst stunted children were significantly smaller and lighter than non-stunted children from birth through 5 years of age, there were no significant differences in daily nutrient intake. Indeed the intakes of all children reflected the relatively high fat/high energy diet characteristic of "western" diets, combined with the high fibre content consistent with the diet of children in developing countries.

It seems likely that stunting is achieved, and alleviated, through a complex series of bio-behavioural factors. It would seem logical that nutrient intake is an important variable within that complex but may not be measured with appropriate sensitivity by food frequency analyses.

Infant diseases in Central Europe during the Neolithic. – P. CARL-THIELE and M. SCHULTZ, Center of Anatomy, University of Göttingen (Germany).

During Early Neolithic Times, when the culture of the Bandkeramik flourished, people in Central Europe began to be sedentary agriculturists. The change in economy implied changes in the living conditions which might have caused new diseases. As children were the weakest members of a prehistoric society, they probably would have suffered from diseases influenced by environmental agents typical of sedentary life.

To check this hypothesis, the skeletons of 98 subadults from the Bandkeramik cemetery of Wandersleben (Thuringia) and of 27 subadults from the Bandkeramik cemetery of Aiterhofen (Lower Bavaria) were examined by macroscopic, radiological, endoscopic, light and scanning-electron microscopic techniques.

The results are striking and characterize the Early Neolithic farmers as a group of people who developed a very specific way of life within a harsh environment. The arguments of some scholars that the economic system in Europe during the Early Neolithic produced a surplus of food appear not to apply in this case. Deficiency diseases (e.g. scurvy) appeared in the foreground, but some inflammatory diseases (e.g. sinusitis) were also frequent. The results demonstrate that malnutrition was apparently the basis for some of the inflammatory diseases. The frequencies of the various diseases observed in these populations reveal a great deal about their health state and characterize the living conditions in the Neolithic Age as not having been very favourable.

Dental morphology of the free-ranging mantled howling monkeys on Isla de Ometepe, Nicaragua, and the Nicaraguan collection at the National Museum of Natural History.

G. CARMICHAEL and L. WINKLER, University of Pittsburgh at Titusville.

Although the mantled howling monkey has been widely studied in most areas of its range, there have been few studies of the populations in Nicaragua. One of these previous studies identifies several distinctive dental wear and loss patterns (Smith et al., 1977). Approximately 10% of the sample have extensive attrition

on their teeth (half of these are from the island of Ometepe) and the majority of teeth lost are the lower anterior teeth.

The present study examines the dentition in a population of mantled howling monkeys on the island of Ometepe in Nicaragua. Dental impressions (3-M express, triple-tray) have been taken from 10 animals (5 males, 5 females) that were anesthetized as a part of a capture/release project (Winkler et al., in prep). The dental wear, tooth and morphology of the overall dentition and of individual teeth were examined in situ and from casts. Twenty percent of the male howling monkeys of the study group had loss or attrition of the upper and lower incisors whereas the females had no loss of these teeth but had extensive wear. Several of the males showed distinctive bilateral C¹ wear differential with one side substantially more worn than the other (right incisor had been fractured and extensively decayed in one male). Premolars wear was more common than molar wear (extensive molar wear was noted in only one animal). Dental heights and wear patterns from this island population were compared with some of those from the earlier study (Smith et al., 1977). Only 7% of the males in this earlier study (all from the mainland) had incisor loss but a substantially higher number showed extensive molar wear (20%). Some of these males also had the same pattern of differential canine wear as the study population.

As noted in the Smith et al., (1977) study, howling monkeys on the island of Ometepe show unusual attrition patterns. We concur that this may be due to the geological nature of Ometepe whereas substantial volcanic dust is ingested with food sources. However, the distinctive canine wear patterns may be related to the use of these teeth in male-male aggression. Several of the study group males showed substantial scarring, including one male with a bite wound on its right side of the face. These, possible dietary factors contribute to some of the differences observed between the Ometepe and mainland monkey populations, will be discussed.

The assistance of Ometepe Biological Field Station, Dr. Richard Thorington and Linda Gorman of the National Museum of Natural History, Dr. Greg Peter and Dr. Rex Sohi is greatly appreciated.

Axial rotation in the lumbar vertebral column of *Australopithecus africanus*. M. CARTMILL and D. SCHMITT, Duke University Medical Center, Durham, NC 27710.

Counter-rotation of the thorax and pelvis is important in human bipedalism. The long lumbar vertebral column and wide pelvis of australopithecines suggest that vertical-axis rotation was even more important in early hominids. To evaluate this possibility, we measured variables that govern lumbar vertebral rotation in *Homo*, *Pan*, and *Australopithecus* (specimens and casts of AL-288, Sts 14, Stw 431, and SK 853).

Axial rotation or twisting in the upper part of the human lumbar vertebral column is severely restricted by the parasagittal orientation of the zygapophyseal facets. In the lower lumbar region, a more dorsal facet orientation facilitates rotation. *Pan troglodytes* exhibits a more constant, intermediate degree of dorsality in facet orientation throughout the lumbar vertebral series. Like Sander (1998), we find that facet orientation in *Australopithecus africanus* from Sterkfontein is chimpanzee-like in the upper lumbar vertebrae and human-like in the lower lumbar. Although axial rotation between L6 and the adjoining vertebrae is limited in *A. africanus* by a specialized lateral displacement of the zygapophyseal facets, rotatory mobility is otherwise facilitated throughout the lumbar column by several mechanisms, including the orientation of those

facets, their planar shape, the increased number of lumbar vertebrae, and the relatively small diameter of the intervertebral disks.

These facts contradict the claim that counter-rotation of the thorax and pelvis was more limited in australopithecine locomotion than in human bipedalism. The long, flexible lumbar column of *A. africanus* argues against a specifically apelike arborealism in this form (although it does not preclude extensive arboreality). However, our findings provide additional support for Rak's thesis that vertical-axis rotation played a more important role in the locomotor behavior of australopithecines than it does in either human or ape locomotion.

This research was supported by a grant from the L.S.B. Leakey Foundation.

Frequency and form of the supracondylar spur trait in ancient Nubians. D. T. CASE and S. E. BURNETT, Department of Anthropology, Arizona State University, Tempe, AZ 85287-2402.

The supracondylar spur is an infrequent non-metric trait found on the medial aspect of the distal humeral diaphysis. It ranges in size from a low fin of bone rising only slightly above the smooth surface of the humeral shaft, to a long, distally curving spur sometimes measuring two centimeters or more. The spur is believed to be an atavistic trait in humans reflecting the evolutionary remnants of an entepicondylar bridge found in several mammalian taxa, including the felids and most mustelids.

There appears to be little information available in the literature about the frequency of this trait in archaeological samples from Africa. Therefore, we examined 509 humeri from 288 ancient Nubian skeletons for presence of the spur. Two hundred thirty one of these skeletons date to the Meroitic period (350 BC to AD 350), 35 date to the Ballana period (AD 350 to 500), and seven date to the Christian period (after AD 500). The trait was considered present if a visible projection of bone was noted at the proper location on the medial portion of the humeral diaphysis. In addition, since the mammalian homologue of the supracondylar spur involves a complete bony bridge between the medial epicondyle and the humeral diaphysis, we examined the medial epicondyle of each humerus for presence of the trait as well.

The trait was identified in its standard location in four individuals. A fifth individual exhibited a bony projection rising from the medial epicondyle of her left humerus. This projection is tubular in form and rises approximately seven millimeters antero-proximally from the epicondyle's anterior surface. Three of the affected individuals date to the Meroitic Period and two, including the individual with the affected medial epicondyle, date to the Ballana period. Including this fifth individual, 1.7% of the Nubians in the sample exhibited the trait.

Changes in Population Structure in Late Pleistocene Eurasians. RACHEL CASPARI and JOHN HAWKS, Paleoanthropology Laboratory, Department of Anthropology, University of Michigan, Ann Arbor MI 48109-1382.

An understanding of population structure of prehistoric peoples is a prerequisite to the reconstruction of genetic histories. Different reconstructions of recent human evolution have different expectations about changes in population structure over time. If the low F_{st} characteristic of humans today is due to the recent origin of our species, F_{st} should have been smaller in the past, increasing as the species diversified. Conversely, if the low F_{st} of modern humans is due to increasing gene-flow between populations one may expect higher F_{st} in the past, decreasing as populations expanded in the Neolithic and came into more frequent contact.

Skeletal data provide independent assessments of prehistoric population structure that can be used to examine changes over time. Relethford showed that F_{st} can be estimated from craniometric data; his results based on osteological variables were comparable to those based on genetic data and he concluded that craniometric data could be used as proxies for genes in some analyses. Using his technique, we have found that dental breadths also yield a comparable F_{st} estimate for living humans. We address the question of whether F_{st} of European/Western-Asian populations has changed between four dental samples: Mousterian, Upper Paleolithic, Neolithic and modern. Each of these samples is subdivided into three geographic populations, Western European, Eastern European and Levantine, and the relationship of between-group variance to the total variance assessed. Our results indicate that F_{st} for past populations in Europe and the Levant has not remained static over time, with a trend toward reduction. We conclude that F_{st} estimates using paleoanthropological data are a promising source of insight about ancient population structure.

Is being Hispanic a Risk Factor for Non-Insulin Dependent Diabetes Mellitus (NIDDM)? B. M. CHAKRABORTY, Community Health Practice Module, and R. CHAKRABORTY, Human Genetics Center, School of Public Health, Univ. Texas Health Science Center, Houston, TX 77225.

Prior epidemiological as well as genetic studies have shown that the populations described as Hispanics have higher prevalence of NIDDM when they are compared with age-sex matched non-Hispanics controls. Such observations raise the possibility of Hispanics being by itself a risk factor of NIDDM.

The objective of this research is to critically assess the basis of this hypothesis. First, it is shown that the descriptions used to define the term Hispanics have both operational and methodological problems. Second, compiling data from genetic and demographic surveys, it is documented that in the US the groups identified by this term are genetically as well as culturally heterogeneous.

Furthermore, epidemiologic data indicate that the actual risk factors of NIDDM also covary with the ethnicity of Hispanics. These considerations lead to the conclusion that by the current definition of the term, being Hispanic may not be a stand-alone independent risk factor of NIDDM. (Research supported by NIH grants GM 41399, and GM 58545).

Role of mixtures of genetic admixture in susceptibility to complex diseases. R. CHAKRABORTY. Human Genetics Center, Univ. Texas School of Public Health, Houston, TX 77225.

Epidemiologic study designs involving migrants have been used to determine the role of genetic factors in susceptibility of complex diseases for several decades. More recently, it has been shown that in admixed populations prevalences of complex diseases follow a predictable pattern of variation with the extent of gene admixture when the contributing ancestral populations have substantial differences of disease prevalence. Furthermore, alleles at genes linked to the disease susceptibility locus (or loci) are also expected to show frequency differences that correlate with disease prevalence in admixed populations as a function of their recombination distance with the susceptibility locus (loci). These considerations form the basis of using admixed populations for designing studies of mapping genes underlying complex diseases.

In this presentation it is shown that the variance component of a quantitative risk factor underlying a complex disease ascribable to a polymorphic genetic marker decays with increasing linkage disequilibrium (LD) between the marker and disease loci. As a consequence, the frequency differences of a threshold disease in individuals of specific marker genotypes reduce with increasing LD between the marker and disease loci. These, together with the decrease of standardized LD with increasing recombination distance, allows the formulation of study designs in using admixture as a means of detecting genes underlying complex diseases. For populations of known admixture history, further refinements are possible by screening polymorphic markers in the genome at which allele frequency differences in the contributing ancestral populations are substantial. Sample size requirements for mapping genes through association studies in admixed populations are determined from the above theoretical predictions. Also, examples of complex diseases are given that characterize situations where specific complex diseases can be studied in various admixed populations for which genome wide markers with population-specific allele frequency differences are documented. (Research supported by NIH grants GM 41399, GM 45861 and GM 58545).

Genetic and phenotypic diversity in Old Order Mennonites. A. CHAKRAVARTI, Department of Genetics, Case Western Reserve, Cleveland OH 44106

The Old Order Mennonites of Lancaster County, PA are the descendants of an Anabaptist group who immigrated to the New World ~ 250 years ago. This closed community represents a genetically isolated population whose current members are related to one another through multiple common ancestors. The Old Order Mennonites have many of the expected genetic features of small populations, such as the high frequency of several recessive lethal disorders. Polymorphism analysis of microsatellite markers across the autosome and X chromosome shows some loss of genetic variation on autosomes but not on the X chromosome. Results of D-loop sequencing of mtDNA also suggests substantial variability. Genetic marker analysis of the Y chromosome shows restricted variation. These results imply that the effective population number of males and females are quite different in the population, with females having made a greater contribution to the population. These findings have several implications for the mapping of multigenic traits in these isolated populations.

Testing the application of phylogenetic taxonomy to fossil hominine taxa using an extant primate model. M. L. CHANG, University of Pennsylvania, Philadelphia, PA 19104.

Analyses of late Pleistocene human phylogeny have relied upon taxonomies of extinct hominine forms for their units of analysis. However, the affinities of many fossils are in question, and changes in taxon definition change the resulting phylogenetic hypotheses dramatically. For this reason, among others, evolutionary trees in the paleoanthropological literature are notoriously unstable.

Cladistic analysis has proven to be effective below the species level for testing population relationships and species identity among extant avian and mammalian taxa (Rising and Avise 1993; Baker et al. 1995; Lento et al. 1997). However, some have questioned the utility of cladistic methods when dealing with intraspecific variation. In addition, because studies on extant forms reveal a discordance between phylogenies drawn from molecular and morphological data, a study assessing the relationship between morphology and other available data used for assessment of population structure is warranted.

The present study explores the use of phylogenetic systematics in testing the validity of fossil hominine taxa using an extant primate model. *Cercopithecus aethiops*, whose range spans much of sub-Saharan Africa, is a well-studied terrestrial species with a subdivided population structure. Genetic, ethological, and biogeographical documentation of the population structure and variation of this species and its subspecies is available to test the effectiveness of cladistic methodology in the presence of varying levels of gene flow.

Metric and nonmetric craniodental characters were recorded from a skeletal sample of *C. aethiops* representing variation in this species over most of its range. The results

of a cladistic analysis using these morphological characters were compared to hypotheses of population relationships formulated using other available kinds of data. The degree of gene flow between groups was estimated using this comparative data and used to assess the effect of admixture on the quality of a phylogenetic hypothesis derived from morphological characters.

The results of this study contradict claims that cladistic methods are ineffective when there is gene flow between taxa. They indicate both opportunities and limitations to applying phylogenetic taxonomy to extinct human groups. These findings suggest a means by which to reconstruct the relationship between genetics and morphology as applied to the taxonomic analysis of later Pleistocene hominine groups, including "archaic sapiens," Neandertals, and Upper Paleolithic *Homo sapiens*.

Hylobatid Systematics: An analysis based on morphological and molecular data. H. CHATTERJEE, I. BARNES and M. THOMAS. Department of Biology, University College London, WC1E 6BT

Several phylogenies have been proposed for the gibbons and siamangs, genus *Hylobates*. Previous studies have used morphological, behavioural and chromosomal characteristics to resolve phylogenetic relationships among hylobatids, but results have proved inconsistent and there remains much controversy. This study uses a combination of morphological and molecular data to resolve some of these controversies, and provides a new phylogeny for the genus. In the first part of this study, over 30 postcranial and 40 craniodental skeletal measurements were collected from museum specimens, representing up to 40 individuals of each of the eleven currently recognised species. Principal Components Analysis of these data shows that species-specific osteological variations are expressed in the orbit, nasal aperture, cranial vault, pelvic proportions and intermembral indices.

In addition, two sections of the mitochondrial genome have been PCR amplified and sequenced: the N-terminal end of the cytochrome b gene and hypervariable region I of the control region. DNA was extracted from non-invasively obtained hair samples from each of the eleven species. Interspecific and intraspecific variations in the sequence data were observed and analysed using maximum likelihood methods. The timings of speciation events were also calculated and considered in relation to palaeobiogeographic change and modes of speciation. Cytochrome b gene sequences were amplified in five species. These sequences were analysed in conjunction with published cytochrome b gene sequences in the six other species. Previous studies have proposed that cytochrome b gene alone cannot resolve the evolutionary relationships among hylobatid sub-genera. A re-analysis of this supposition is offered here. While the results of this study suggest that morphological and behavioural characteristics alone cannot completely resolve phylogenetic relationships among hylobatids, it is proposed that a simultaneous analysis of molecular and morphological characteristics can yield a more accurate and robust phylogeny for the genus.

Preliminary analysis of "Kennewick Man," a Paleoamerican skeleton from the Northwestern United States. J.C. CHATTERS, Applied Paleoscience, 648 Saint St, Richland, WA 99352.

The Paleoamerican skeleton popularly known as Kennewick Man has been inaccessible to open scientific inquiry since shortly after its 1996 discovery. Although complete studies have been prohibited, preliminary forensic analysis was conducted and photographs and a highly detailed cast of the skull were obtained.

The nearly-complete skeleton has a corrected radiocarbon age of 8410±60 (13c -14.0; UCR 3476), which is corroborated by its derivation from an early Holocene floodplain deposit.

The individual is a male. Pelvic and cranial characteristics indicate that death came in middle age, although this is somewhat contradicted by light wear on the third molars and the lack of significant osteoarthritis. Mean stature estimates range from 175 to 178 cm. A crural index of 85 and generally gracile build bespeak a subtropical body type, which differs markedly from the small, robust stature and short distal limbs of modern Northwestern Amerinds.

Premortem traumas are numerous, including a small compression fracture of the left frontal, multiple severely fractured ribs, a possible radial head fracture, and a projectile point wound in the right ilium. The left humerus is macroporous at the septum and is much smaller than the right, which may result from a pinched brachial nerve or extensive atlatl use. Minor osteoarthritis is present in elbows, knees and the spine. A large lytic lesion had developed around the projectile point and shows extensive calus formation. Re-infection may be indicated by secondary perimortem lysis around the projectile and osteomyelitis on the cranium.

Preliminary craniofacial analysis, the lack of platymeria, non-Sinodont dental characteristics, and the subtropical body type distinguish this individual from modern Amerinds. This is consistent with analyses of other early skeletons in North and South America (Steele and Powell 1994; Powell 1998; Neves et al. 1998; Neves and Pucciarelli 1991, Lahr 1997; *contra* Nelson 1998), which indicate that the earliest migrants to the Americas were not of the derived North Asian form.

Non-metric dental variation in remains from a Byzantine monastic community in Jerusalem

J CHEADLE† and SG SHERIDAN††

†Department of Ancient Studies, University of Maryland, Baltimore, MD; ††Department of Anthropology, University of Notre Dame, Notre Dame, IN 46556

Analysis of the remains from a Byzantine monastic complex (AD 460-614) in Jerusalem has yielded over 15,000 skeletal elements. Among the remains are over 2,598 adult teeth. The purpose of this research was to compare the non-metric dental variation of the children and adults from St. Stephen's monastery to determine the degree of relatedness of the two groups.

Teeth were scored using the ASU system (Turner et al, 1991), and only dental variants with a 'scorability index' over 85 were included (Nichol and Turner, 1986). By comparing the distribution of discrete dental characteristics

in subadults with mixed dentition to those of their adult counterparts, this study began to address whether these remains derive from the same core population. Between group variation was assessed using modified Fisher's exact probability (after Greene, 1967, 1972, 1984). There was a significant difference between adults and subadults in all tooth groups, although within group comparisons showed little variation among the subadults.

Approximately one-quarter of the remains from St. Stephen's monastery represent subadults. There is a very rich historical record for the Byzantine occupation of this site, however, no mention of a large concentration of children has been found to date. Some have suggested that: a) these are children from the surrounding community interred at the monastery due to its location near the bones of a saint, b) the monastery served as an orphanage or hospital, or c) they represent young monastics in training (oblates) brought to the monastery on pilgrimage. The within group consistency of the subadult dental traits supports the idea that the remains were derived from a homogeneous, probably local, population. Subsequent analysis of childhood morbidity/mortality indicators should help distinguish between the aforementioned options.

For the adults, the historical texts indicate St. Stephen's was a significant site of pilgrimage, drawing members from as far away as Syria, Russia, Spain, Italy, Constantinople, Egypt, and Mongolia. The degree of adult heterogeneity indicates derivation from a variety of locales, consistent with the historical record.

* This research was supported by the National Endowment for the Humanities, the Albright Institute for Archaeological Research, and the University of Notre Dame's Institute for Scholarship in the Liberal Arts.

Estimating non-Indian genetic admixture in American Indians. Y.-F. CHEN and R.C. WILLIAMS, Department of Anthropology, Arizona State University, Tempe, AZ 85287

Caucasian and African genetic admixture in more than one hundred American Indian populations was estimated using the allele frequencies of 6 blood group loci by both the Weighted Least Squares (WLS) and Chakraborty's (1992) methods. Caucasian admixture was estimated using a dihybrid model, meaning that all genes in the sample are assumed to derive from only two parental populations. African admixture was estimated by the WLS method with a trihybrid model. The 95% confidence interval for the amount of admixture was calculated for each population. The amount of admixture for each population was noted on maps.

For the ABO locus, the A_1 allele has a wide range of frequencies in North American Indian tribes. To accurately calculate the amount of admixture, A_1 and O alleles were combined as though representing a single allele for these populations.

In 60 populations exhibiting genetic admixture, the Pearson's correlation coefficient for the results of both the WLS method and Chakraborty's method is equal to 0.953. The mean difference in the amount of admixture between these two methods was 0.0003, with a standard deviation of 0.0195. For 41 populations (68%), the differences between the two methods were within ± 0.01 , and for 51

populations (85%), the differences between the two methods were within ± 0.02 . These data indicate that the two methods produce consistent results. Cavalli-Sforza and Bodmer's (1971) method is also useful to estimate the amount of admixture. However, when the frequencies of both the hybrid population and one parental population for an allele are equal to either 1 or 0, the amount of admixture cannot be calculated by their method.

Population-specific histological age estimating method: a test. H. CHO, M. STREETER, and S.D. STOUT, University of Missouri, Columbia, MO 65211.

The population-specific histological age-estimating formula for African- and European-Americans developed by Cho and Stout (1997 AAPA) was tested on independent samples of modern African- ($n=40$) and European- ($n=40$) American ribs. The results indicate that the population-specific formula (Cho and Stout, 1997) is a better predictor of age than the non-ethnic-specific formula of Stout and Paine (1992). The advantage of the population-specific formula is especially evident for older individuals (>40).

These results are consistent with previous findings from Cho and Stout (1997) that Osteon Population Density (OPD) differs most significantly between African- and European-American samples after the fourth decade ($p<0.0001$). Therefore, a population-specific formula is recommended when ethnicity is known.

Genetic and environmental correlations between various anthropometric and blood pressure traits among Samoans. A.C. CHOH Department of Anthropology, University at Albany, SUNY, Albany, New York, 12222.

The concomitance of many chronic disorders such as obesity, hypertension, diabetes and cardiovascular disease has led many to the conclusion that these diseases are genetically linked. The possibility that simple Mendelian control of these phenotypes appears remote, however, advances in computer technology allows investigators to search for more complex patterns of inheritance. In particular, pleiotropic effects can now be examined through the use of bivariate analyses. This study investigates the genetic correlations between various anthropometric and blood pressure traits among Samoans.

The data consist of anthropometric and blood pressure data collected in Western Samoa, American Samoa and Hawaii from 1975 to 1982. They include information on Samoans in 801 pedigrees. Univariate and bivariate heritabilities as well as genetic and environmental

correlations of weight, height, body mass index (BMI, weight (kg)/ stature m³), diastolic blood pressure (DBP), systolic blood pressure (SBP), triceps skinfold, subscapular skinfold, centripetal fat proportions (CFP, [subscapular/subscapular+triceps] * 100), subscapular triceps ratio (STR, subscapular/triceps * 100) and sum of skinfolds (triceps+subscapular) were estimated using maximum likelihood methods with the computer program Pedigree Analysis Package (PAP).

The analysis indicates that significant heritable components ($p < 0.05$) exist for weight (46%), height (58%), SBP (29%), DBP (33%), triceps skinfold (51%), subscapular skinfold (51%), BMI (40%), and sum of skinfolds (53%), but not for CFP and STR. 22 out of 28 phenotype pairs share significant environmental effects, while 25 of the 28 phenotypic pairs share a significant genetic effect. The genetic correlation between SBP and DBP is 0.949, while the environmental correlation is 0.766. Genetic correlations between blood pressures and skinfolds range from 0.483 to 0.561, while the environmental correlations range from 0.231 to 0.335. These and other results will be presented and discussed.

This work was supported by NIH grants AG09375, HL52611 and NSF grant SBR-9512290.

Anthropometric variation in North-Central Mexico. A.F. CHRISTENSEN, Augusta State University, Augusta, GA 30904.

Anthropometric data from five indigenous Mexican groups, collected by Carlos and Manuel Basauri in 1933, were reanalyzed using RMET (Relethford, 1996). Two of the series, Huichol and Tarascan, could be subdivided by locality, the others could not; analyses were performed with these series lumped and split. Male and female cranial (10) and postcranial (14) measurements were considered separately. A Mantel test revealed few correlations significant at the 0.05 level between any of the anthropometric matrices and geographic or linguistic distances. However, the two groups which were closest linguistically and geographically, the Cora and Huichol, were also close biologically. The other three groups, Tarascan, Azteca, and Otomi, were not closely related to each other or the Cora-Huichol pair. Bias-corrected r_0 or F_{ST} values ranged from 0.023 and 0.040, for the lumped and split samples respectively, to 0.049 and 0.066. Use of a lower heritability than 1.0, which would be necessary to make these estimates comparable to genetic ones, would produce higher values, but these can be compared directly to other anthropometric studies. These are not dramatically higher than the r_0 of 0.040 reported by Relethford (1991) from seven Irish populations located within 120 km of each other. Given the degree of linguistic differentiation among the Mexican populations, not to mention the different Colonial histories of the communities sampled, this result is surprisingly low. More interesting than the relationships between populations in this case are those within them. The Aztecs of Tuxpan, Jalisco, who were isolated

on the periphery of New Spain, exhibit high r_{ii} values and lower-than-expected phenotypic variance, suggesting the pronounced action of genetic drift. The Otomi of Ixmiquilpan and Cora of the Sierra de Nayarit, despite their very different histories, both exhibit low r_{ii} values and higher-than-expected phenotypic variance, indicating a high level of gene flow. Despite the phenotypic similarities between the Cora and Huichol, their residual variance is very different; this difference matches serological estimations of relative European admixture.

Morphological variation in the upper respiratory tract and airflow dynamics. S.E. CHURCHILL, L.L. SHACKELFORD, J.N. GEORGI and M.T. BLACK, Duke University, Durham, NC 27708.

The climatic correlates of nasal skeletal and soft tissue variation have been of long standing interest in physical anthropology. A number of features in the human nose have been argued to enhance airflow turbulence, thus increasing the exposure of moving air to the nasal mucosa and facilitating heat and moisture exchange in cold and/or dry climates. These features include: an inferior orientation of the nares; a nasal sill that is high relative to the floor of the internal nasal chamber; a nasal valve that is small in cross-sectional area relative to that of the internal chamber; and large, projecting conchae.

To test these claims we studied airflow across physiological flow rates using water and dye flowing through anatomically accurate acrylic models of human nasal air passageways (with adjustment of water flow rates to maintain dynamic similarity). The models were derived from direct casting of the nasal passageways of 10 Caucasian ("leptorhine") cadavers (6 male, 4 female). Measures of naris angle, relative nasal sill height, nasal valve and internal chamber cross-sectional area, and conchal projection were taken directly on the resulting casts. The relationships between aspects of nasal morphology and turbulent air flow were evaluated by examining the flow regimes (laminar versus turbulent) at varying flow rates, with the expectation that the greater the development of the proposed turbulence-enhancing features the slower the flow rate at which flow would shift from a laminar to a turbulent regime.

Naris angle was the only variable that significantly affected the flow rate at which flow became turbulent, with more inferiorly directed nares producing turbulence at slow flow rates. Relative nasal valve area was moderately (but non-significantly) positively related to turbulence, contrary to expectations about nasal valve function derived from previous physiological studies. We also detected a weak negative (but non-significant) relationship between relative conchal projection and turbulence. Variation in the relative height of the nasal sill appears to have no appreciable effect on airflow dynamics.

New *Amphipithecus* from the middle Eocene of Myanmar: Implications for stem anthropoid origins. RUSSELL L. CIOCHON, Dept. of Anthropology, University of Iowa, Iowa City, IA 52242, PATRICIA A. HOLROYD, U.C. Museum of Paleontology, Berkeley, CA 94720, TIN THEIN, Dept. of Geology, University of Taunggyi, Southern Shan State, Myanmar

In April 1997, Burmese researchers recovered two lower jaws of *Amphipithecus mogaungensis* from variegated mudstones within fluvial beds of the Pondaung Fm. NMMP 6 is a partial left mandible with relatively unworn M1-M2, from Mogaung NW, not far from where Barnum Brown found the type. NMMP 7 is a complete mandible with all posterior teeth and aveoli for all anterior teeth, from Bahin, a new locality in the southern Pondaung range.

Together these new specimens exhibit an A-P abbreviated D-V deep symphysis, vertically implanted lower incisors, large projecting canines, P3-4 slightly exodaenodont and obliquely oriented, M3 trigonid appreciably wider than talonid and hypoconulid lobe on M3 reduced M-D, and B-L. Based on these and other characters, *Amphipithecus* lies closer to the undisputed anthropoids of Africa than any other primate in Asia.

Recognition of *Amphipithecus* as the sister taxon of the "telanthropoids" provides compelling arguments for an Asian origin of Anthropoidea. It now seems clear that by the middle Eocene, Asia was host to the two sister taxa of African anthropoids (*Amphipithecus* and *Eosimias*), the probable sister taxa of Anthropoidea (tarsiids and omomyids), and several adapid subfamilies (Protoadapinae, Adapinae, and Notharctinae). This biogeographical distribution strongly suggests that the origin of Anthropoidea, if not all Primates, lies in Asia.

Funding provided by UI International Travel Grant Program, U.C. Museum of Paleontology and Office of Strategic Studies, Ministry of Defence, Yangon.

Occupational Stress and Trends Toward Asymmetry in Two African Skeletal Populations. C. S. CLARK, New Mexico State University, Las Cruces, New Mexico, 88001.

Occupation and the physical stresses associated with it play an influential role in the development and growth of the skeleton. These stresses may manifest themselves in bone anomalies such as skeletal asymmetry, bone degeneration, bowing of the long bones, reshaping, and in diseases such as osteoarthritis and osteoporosis.

This study reports an investigation of occupational stress markers carried out on a population of 120 male

skeletons housed in the University of Pretoria skeletal collection. The dates of death ranged from the early 1980's to the mid 1990's. Previous analysis had identified 60 of these to be of white/Dutch decent and 60 to be of black/African decent. Information was also available on the cause of death, age at death, donation status, and the tribal affiliation of the individuals of African decent. A series of standard postcranial measurements were taken to determine degree of asymmetry and visual inspection was used to identify anomalies. The two populations were then compared for frequency and degree of asymmetry, frequency of anomalies, and degree of general skeletal robusticity.

Preliminary results yielded information that could be expected of a hierarchical social system. Those skeletons of Dutch decent showed less robusticity and fewer signs of intense muscle development than those from the various African tribes. Further, those skeletons of African decent displayed greater degrees of skeletal anomalies such as osteoporosis and osteoarthritis. These preliminary results support the hypothesis that socio-economic status plays an important role in the growth of the skeleton.

Assessment of the howling monkey (*Alouatta palliata*) population on Hacienda La Pacifica, Guanacaste, Costa Rica. M.R. CLARKE, E.L. ZUCKER, C.M. CROCKETT and M. ZALDIVAR, Dept. of Anthropology, Tulane University, New Orleans LA 70118, Loyola University New Orleans, Washington Regional Primate Research Center, and Universidad de Costa Rica.

A complete survey of the forests of Hacienda La Pacifica was done in July and August, 1998 to assess the present howling monkey population and to compare the results with earlier surveys. Methods were identical to the 1991 survey, including an initial transect survey with all 6 field workers (8 days) and two repeat surveys (10 days); three teams of two workers searched smaller areas on consecutive days to relocate and identify animals.

The total population, from the complete survey, was almost identical to 1991 (369 vs. 370). Mean group size was 10.1 (365 animals in 36 groups), which was less than the 1991 mean (12.6). Modal group size was the same (12). Group sizes in 1998 ranged from 4 to 28. Four solitary animals also were found.

There were changes from 1991 in the age-sex composition of groups. There were 19% fewer adult males (55 vs. 68 in 1991) and fewer males per social group. There were 17 one-male groups, 18 two-male groups, and only one three-male group. Fewer adult females were located (168 vs. 183 in 1991; 8% decrease), whereas there was a 58% increase in juveniles and infants (133 vs. 84 in 1991).

This howler population (total number) has been stable since 1974-76, but the pattern of increased number of social groups, noted in the 1984 and 1991 surveys, continues. In this survey, fewer adult males

were located, while the reproductive base of adult females was reduced only minimally. Retention of immatures could be due to changes in arboreal migration routes. Forests have been altered by canal construction and the conversion of pasture land to wet rice production.

Supported by National Geographic Research Grant #6244-98 and the Roger Thayer Stone Center for Latin American Studies at Tulane University.

The ontogeny of sexual dimorphism in the hyoid bone.
MARGARET CLEGG and LESLIE C. AIELLO.
Department of Anthropology, University College
London, Gower St. London WC1E 6BT.

The role of the hyoid bone in supporting the tongue and acting as an attachment site for many of the muscles used in speech gives it an intimate relationship with language. The hyoid bone is unique in that its greater horns do not fuse to the body until middle age, 41-55 years in males and 44-64 years in females. This would allow hyoid growth to continue into late middle age and well after the closure of the last closing epiphyses, the clavicle.

This study explores the growth and variation of the hyoid in males and females from early adolescence to old age. Over 70 hyoid bones of known age individuals, aged 8 years to 93 years, from several modern populations, including the Spitalfields collection at the Natural History Museum London, St. Barnabas Church London and Modern Londoners (departments of Anatomy and Laryngology UCL) were measured. Measurements used included, maximum diameter of the hyoid, maximum length in the sagittal plane, maximum diameter of the hyoid body, maximum height of the hyoid body, hyoid body thickness and length and width of the great horns.

Analysis of these measurements show sexual differences between male and female hyoid bones in adults (>50 years). In particular, male hyoids are much more variable in body thickness and great horn length than are female hyoids. In younger females (<50 years) hyoids, and particularly the hyoid body diameter, show continuous growth until fusion occurs. Male growth follows the same trajectory until late adolescence (c. 18 years). At this time the extreme variation in both size and shape of the male hyoid appears. Explanations for this variation may include the age at which puberty occurs, duration and/or intensity of the adolescent growth spurt. The morphology of the Kebara hyoid is discussed in the context of this modern human hyoid variation.

Soft tissue asymmetry of the human hand: A pilot study. C. N. COAN, Univ. of Massachusetts, Amherst, MA 01003.

Previous inquiries into the relationship between morphology and handedness have concen-

trated on bone, as assessed through linear dimensions, musculoskeletal markers, or density. Studies of soft tissue have been conducted on nonhuman primates, but apparently not on humans, and not in relation to handedness. Yet if muscle tissue responds to use by increasing in cross-sectional area, and if bone tissue, as assessed by various measures, reflects hand use, then the muscle tissue itself ought to be heavier on the dominant side. Thus, for individuals of unknown hand dominance, one would predict that 85-90% should have greater muscle mass on the right hand.

Do modern humans exhibit soft tissue asymmetry of the hand, and if so to what degree, with what consistency, and in what kind of patterns? Do soft tissue differences accord with those observed in linear dimensions or density of bone? Does the pattern of asymmetries among individual muscles or groups of muscles (e.g., thenar, hypothenar) provide clues as to the contribution of handedness to musculoskeletal development?

This pilot study compares right and left hands of a small (n=10) cadaver population, using several different methods of analysis. These include (1) dry muscle weights of seven intrinsic hand muscles; (2) direct bone measures, principally of metacarpals; and (3) linear dimensions and relative bone densities derived from radiographs.

Preliminary analysis suggests both muscle mass and skeletal measurements are greater on the right hand. Radiographic measurements can be problematic. Detailed analysis of results from the various methods will be presented, with particular attention to how methodology affects results.

Paradigms and definitions in early hominid locomotion research. K.E. COFFING, Department of Anthropology, University of California at Los Angeles, Los Angeles, CA 90095-1553

Lately there has been renewed interest in the concept of scientific paradigms, particularly as originally conceived by Thomas Kuhn (e.g., 1962). Recent work includes that of Clark (1993), who applied Kuhn's ideas on scientific paradigms to prehistoric archaeology, and papers by Willermet and Clark (1995) and Smith and Harrold (1997), who considered the applicability of scientific paradigms to the dispute about modern human origins. Not all have agreed on the applicability of Kuhnian paradigms, including Smith and Harrold, who assert that "subparadigmatic struggle" would be a more accurate label for the dispute about modern human origins. Regardless of the true level of a dispute (paradigm, subparadigm, etc.), the *concept* of a scientific paradigm clash has intriguing applications for paleoanthropology. This paper is a consideration of paradigms and paradigm clashes in the controversy over early hominid locomotion.

Early hominid locomotion research has been disputatious for many years. Two positions have been the most vociferously argued. Researchers holding the first of these positions assert that the morphology of early hominids such as *Australopithecus afarensis* included features that "rendered [their bones] virtually incapable of pongid-like function" (Latimer and Lovejoy, 1990, p. 22). They also

assert that "a completely terrestrial habitus was unquestionably responsible" for their morphology (Latimer and Lovejoy, 1989, p. 385). In contrast, those holding the second position consider *A. afarensis* individuals to have been "part-time arborealists" who "could not have survived full-time on the ground" (Susman *et al.*, 1984, p. 150).

A shared concept of how natural selection shapes the morphology of organisms would seem essential for reaching agreement on any evolutionary question. However, the literature on early hominid locomotion reveals that the two opposing camps appear to differ in several fundamental aspects of their concepts of natural selection. The two camps also seem to differ in their definitions of certain important terms commonly employed in early hominid locomotion research. These fundamental differences may or may not be paradigmatic in the strict Kuhnian sense, but they do help elucidate why each side interprets the same fossil evidence in remarkably conflicting ways.

Morphometric recognition of shape-conservative anatomical complexes. TM COLE III, University of Missouri, Kansas City, MO 64108; VB DELEON, S LELE, and JT RICHTSMAYER, The Johns Hopkins University, Baltimore, MD 21205.

Many morphometric studies of primates focus on recognition of anatomical complexes that exhibit significant interspecific variation. The reason is that we are often interested in the most variable aspects of interspecific morphology because they may reflect a corresponding spectrum of adaptive strategies. However, there are often cases where the recognition of relative constancy of form may be just as important. We introduce a method of recognizing such "shape-conservative" anatomical complexes when form is measured using two- or three-dimensional landmark coordinate data.

We have adapted ideas about shape comparison that are frequently used in molecular biology and pharmacology. We use a clique-building algorithm (similar to those used for automated searches of molecular databases) to identify subsets of landmarks where shape is relatively invariant. We also demonstrate that commonly used superimposition (Procrustes) methods are unsuitable for this purpose.

We present two examples where we search for structural commonality in morphologically heterogeneous samples. The first example focuses on conservative aspects of three-dimensional shape in the crania of living atelines. The second example compares mandibular shape in normal mice to shape in a segmentally trisomic mouse model (Ts65Dn) for Down syndrome (trisomy 21) in humans. We conclude by considering the potential usefulness of our methods in comparing theoretical morphologies with databases of real organisms.

Supported in part by a National Research Service Award (NIDR) to JTR.

Stratigraphic consistency in hominin phylogeny. M. COLLARD, University College London; C. A. LOCKWOOD, Institute of Human Origins, Arizona State University; and B. A. WOOD, George Washington University, Washington, DC.

Cladistics is the preferred method of phylogenetic reconstruction in palaeoanthropology. However, cladistic analyses of hominins have to date yielded conflicting, weakly-supported hypotheses of relationship. Recent studies suggest that these problems may be attributable to the type of evidence normally employed in hominin phylogenetic relationships, namely craniodental observations. It is therefore prudent to seek additional lines of evidence. Here, we examine how incorporating temporal information affects estimates of hominin phylogeny. First appearance dates of taxa should be consistent with the sequence of clade origination. Error in appearance dates is unlikely to be greater than the error involved in the phylogenetic analysis of the available morphological data.

We use the Stratigraphic Consistency Optimality Criterion (Huelsenbeck, 1994) to incorporate temporal information. This method essentially lengthens each phylogeny by the degree to which it is inconsistent with the temporal ordering of hominin taxa. Morphological character data were taken from Wood (1992), Lieberman *et al.* (1996), and Strait *et al.* (1997). The order of taxon appearance is *A. afarensis*, *A. africanus*, *P. aethiopicus* & *H. rudolfensis*, *P. boisei* & *H. habilis*, *P. robustus*, *H. ergaster*, *H. erectus*, and *H. sapiens*.

The distribution of putative synapomorphies is generally consistent with the order of species appearances. Nonetheless, the cladograms favoured by Huelsenbeck's method do not perfectly match those supported by analyses of morphological characters alone. The shortest cladograms estimated from the Wood (1992) and Strait *et al.* (1997) data sets differ from the conventional ones in placing *H. rudolfensis* as the sister group to all other *Homo*. For the Wood data set, *H. erectus*, not *H. ergaster*, is the sister group of *H. sapiens*. Two cladograms were favoured for the Lieberman *et al.* (1996) characters. The first resembles the shortest cladograms from the other data sets. In the second, *Paranthropus* and *Homo* are paraphyletic, with *P. aethiopicus* and *H. rudolfensis* occupying more basal positions in hominin phylogeny.

The main implications of these analyses concern the pattern of character evolution associated with the origin of the genus *Homo* and whether *H. habilis* can validly be interpreted as the most primitive species of this genus.

Supported by the Wellcome Trust and the Henry Luce Foundation.

Biogeography and evolution in spider monkeys (*Ateles spp.*). A.C. COLLINS, Dept. of Anthropology, University of Wisconsin, Madison, WI. 53706

Phylogenetic relationships among populations of spider monkeys (*Ateles*) were investigated using mitochondrial DNA sequence variation to identify four suggested species of *Ateles* (Collins and Dubach, in prep.) These species include *A. paniscus* (the former subspecies *A. p. paniscus*); *A. belzebuth* (which includes *A. b. marginatus*, *A. p. chamek*, and *A. b. belzebuth*); *A. hybridus* (the former subspecies *A. b. hybridus*); and *A. geoffroyi* (which includes all subspecies of *A. geoffroyi* and the former species *A. fusciceps*). This arrangement is similar to the taxonomy of Froehlich *et al.* (1991) based on discriminant analysis of cranio-dental morphology.

This presentation examines the biogeography and evolutionary mechanisms that acted to produce these *Ateles* species. Recent hypotheses have suggested that a great deal of speciation occurred among Neotropical primates during the Pleistocene. Through mechanisms such as Pleistocene forest refugia formation, which was stimulated by changes in temperature and precipitation due to glacial fluctuations and the changing pathways and size of Amazonian rivers.

This research investigated phylogenetic relationships and implied biogeography for a very widely distributed Neotropical primate to examine taxonomic relationships and possible factors which promoted differentiation. Through the use of a local molecular clock applied to genetic distance measures between clades, this study was able to determine likely dates for the last common ancestors of each major clade. Combining this information with suggested recreations of the paleo-biogeography of South and Central America, this study was able to propose likely mechanisms which were causal agents in *Ateles* speciation. Contrary to prevailing theories for many Neotropical primates, most of the speciation in *Ateles* occurred in pre-Pleistocene environments and is likely due to major changes in geological features.

This study proposes that much of the speciation in *Ateles* occurred between 3.2 and 2.0 million years ago and was due to allopatric speciation driven by features such as the final uplift of the Andes Mountains, fluctuations in the size of the lower Amazon River, and the unsuitable environments of the Guianian Highlands. Only in the formation of *A. hybridus* is Pleistocene forest fluctuation and refugia formation, a possible explanation for speciation. Additionally, Neotropical rivers, with the exception of the Amazon, seem to present limited barriers to gene flow in *Ateles*. Differences between black-water and white-water drainages and their associated flora are more important factors affecting gene flow in *Ateles*.

Establishing resolution in paleohabitat reconstructions with relevance to hominid adaptations.

S.R. COPELAND, Anthropology, Rutgers Univ.

Currently available paleoenvironmental reconstructions of early hominid habitats, such as those based on faunal remains or paleosol carbon isotopes, define the relative proportions of closed versus open vegetation at particular fossil localities. However, exactly what these structurally-defined categories mean in terms of hominid adaptations, including their effects on feeding, ranging, and refuging behaviors, is not addressed in such studies, and has not been well-documented. Since vegetation structure would have directly influenced hominids in terms of the availability of 1) arboreal refuge, and 2) plant foods, I conducted a study of the relationship between these factors and general vegetation structure, soil types, and geomorphological settings in a variety of modern habitats in Serengeti and Lake Manyara National Parks, Tanzania.

As would be expected, there is a general, positive correlation between tree cover and arboreal refuge, but there are several important exceptions. For example, the types of trees in the ground water forest at Manyara create an entirely different and arguably better suite of potential refuges than those in a dense patch of *Acacia xanthophloea* woodland. Furthermore, those two types of dense tree cover should be distinguishable in the geological record at specific paleolandscapes localities due to differences in soil chemistry and grain size. While the

abundance of plant foods positively correlates in a general way with increasingly closed habitats, there are unique plant food types available in different physiognomic and pedological situations. For example, ground-level fruits are abundant in bushlands, but tree canopy-level fruits are seasonally present in the forest.

These and other examples show that hominid adaptations do not correspond merely to a gradient of open to closed vegetation types. Based on these modern analog studies, other features at fossil localities, such as paleosol types, geomorphological settings, and local hydrological situations, can be used in conjunction with traditional paleoenvironmental indicators to create richer vegetation reconstructions that are more meaningful in terms of potential hominid adaptations.

Supported by grants from NSF and CHES at Rutgers.

The Pleistocene-Holocene transition in Italy. The contribution of the morphological dental traits. A. COPPA, A. CUCINA, R. VARGIU, Università di Roma "La Sapienza", Italy; D. MANCINELLI, Università di L'Aquila; M. LUCCI, Università di Sassari, Italy.

Aimed at analyzing the relationships among Italian populations with a diachronic approach, we compared morphological dental traits of two samples from Upper Paleolithic-Mesolithic (63 individuals) and Neolithic (273 individuals) periods with numerous samples (6,500 individuals) spanning from the Copper to Medieval age. Thirty-three morphological traits were scored following the ASU System. These data were used to build maximum likelihood trees, whose robustness was tested by bootstrap, and Principal Component plots. Results provided by the two methods were very similar each other. The Upper Paleolithic-Mesolithic sample was found to be markedly different from the others. At the same time, it branched off from the same node (supported by 90% of bootstrap replicates) of the Neolithic sample. This may indicate an Upper Paleolithic genetic component in the Neolithic populations. The Bronze age (early, middle and late), Iron age (early, middle and late) and recent samples (roman imperial, *tardo antico* and medieval) fell into three separate clusters. On the whole, there is a marked similarity between samples belonging to the same chrono-cultural *facies*, which suggests a common origin and/or a high level of interbreeding. Furthermore, we observed an overall congruence between chrono-cultural sequence and topology of the tree, with the Copper age group being the only exception. The similarity among recent samples shows that the biological (genetic) structure of the Italian population went definitively under a stabilization process during the Roman Empire. We speculate that this preliminary results provide evidence of a certain biological continuity in the peopling of the Italian Peninsula from Paleolithic to historical times. We identified a set of twelve high- and nine low-frequency features that allow distinguish Paleolithic/Mesolithic sample from all of the others, and was accordingly termed "Upper Paleolithic/Mesolithic Dental Complex". This is characterized by the following features: absence of shovel shape and double shovel shape of central and lateral upper incisors, parastyle in all upper molars, agensis and peg shape in the third upper molar, cusp 7 in all lower molars; high frequency of the interruption groove in the upper lateral incisor, cusp 5 in the second and third upper molars, Carabelli's cusp in the third upper molar, two-rooted upper first premolar, Y-groove pattern in the third lower molar, 4 cusps in the second and third lower molars, trigonid crest in the second and third lower molars.

This work was supported by the "Progetto Finalizzato CNR, Beni Culturali" 96.01106.PF36 and 97.00623.PF36, MURST 40%/97.

Investigating the relationship between social roles and dental disease: variation within Ontario Iroquoian ossuary populations. C.M. CRINNION, Department of Anthropology, McMaster University, Hamilton, Ontario, Canada, L8S 4M1.

Several key findings are discussed from an MA project designed to compare the dental disease affecting separate demographic groups within one community. Mandibles and maxillae were examined from 158 adults interred at the Uxbridge (BbGt-1), Kleinburg (AlGv-1) and Syers (no Borden designation) ossuaries. Individuals were included based upon their preservation, averaging only 50 percent postmortem tooth loss. These people lived during the Late Ontario Iroquoian period (circa AD 1350-1600), subsisting on a diet of maize, beans and squash cultigens, fish, wild game, and an assortment of wild fruits and vegetables. There is no evidence for any mechanical cleansing of teeth by this cultural group from either the ethnohistoric literature or skeletal studies.

As expected for their subsistence economy, most individuals exhibited high levels of dental disease, as determined by caries, pulp exposures, abscesses and antemortem tooth loss. With few exceptions, the females scored higher than the males for the Diseased-Missing Index, the Observed Caries Rate and the Corrected Caries Rate (Lukacs 1995). In general, variations in dental disease are primarily caused by the chemical qualities, texture and amounts of foods eaten, and the frequency and duration of meals. Thus, these results indicate that the adult males and females in these three Iroquoian communities practised different eating habits on a regular basis. It is probable that their daily activities determined access to certain types of foods and the number of meals eaten.

Additionally, the results from independent age and sex estimations indicate a younger mean age at death for the females than for the males in these three samples. Iroquoian women may have been inadvertently placed at a higher risk for long-term dental disease, with the potential for subsequent widespread infection, a depleted immune system and terminal illness.

Phylogenetic relationships among *Saimiri* species based on nuclear and mitochondrial DNA evidence. S. CROPP, University of Chicago, Chicago, IL 60637, and S. BOINSKI, University of Florida, Gainesville, FL 32611.

The taxonomy of squirrel monkeys (genus *Saimiri*) has been, and continues to be, the subject of much debate, with various authors proposing anywhere from one to seven species. Although a large number of behavioral and cytogenetic studies have clarified similarities and differences among various squirrel monkey taxa, until recently, very little was known about the phylogenetic relationships among members of the genus. Also, while the divergence of *Saimiri* from other New World genera has been estimated at 16.5 to 19.0 MA, divergence times among the extant species have not been well established. This study examines the phylogenetic relationships

among *Saimiri* taxa based on DNA sequence data and uses that data to estimate divergence times among them.

DNA sequence data was collected from four regions of the genome: the D-loop and cytochrome *b* regions of the mitochondrial DNA, intron 1 of the IRBP gene, and intron A of the ZFX/ZFY gene. Six *Saimiri* taxa were included in this study, as well as a sample of *Cebus* sp., which was used as an outgroup reference taxon.

Parsimony analysis of the sequence data revealed approximately equal amounts of genetic diversification between *S. sciureus*, *S. boliviensis*, and *S. oerstedii*. Based on the sequence data, the Costa Rican squirrel monkey, *S. oerstedii*, appears to be most closely related to the northern squirrel monkey, *S. sciureus*. Although this relationship is not well-supported in a bootstrap analysis, combining the DNA sequence data with behavioral and morphological data yielded extremely high support for this relationship. The poorly studied *S. ustus* was included also in this study and was found to be more genetically differentiated than the other squirrel monkey taxa. Divergence times between the species were also calculated.

Results of this analysis have important implications for the use of squirrel monkeys in biomedical research, for interpretations of behavioral and morphological data, and for the taxonomy of the genus.

This work has been supported, in part, by an Alfred P. Sloan Postdoctoral Dissertation grant.

How reliable are the skeleton indicators for subadult's age at death estimation? A test with the Coimbra Identified Skeletal Collection. E.CUNHA; F.MAGALHÃES and A.ABADE, Departamento de Antropologia, Universidade de Coimbra, 3000 Coimbra, Portugal

It is well known that the estimation of subadult age at death from skeletal samples is more accurate than age estimation of adults. Nevertheless, the exact reliability of each of the widely used methodologies is not known. Taking into account that the techniques used are group-specific and are derived mainly from samples of white North American and northern European children, their reliability on other skeletal series is uncertain. The possibilities of testing their efficiency are rare because of the unavailability of non-adults in identified skeleton collections. The Museum of Anthropology, Coimbra University, Portugal, has an identified skeletal collection including 64 subadults (with ages at death from 7 to 21 years). We decided to test some of the subadult age estimation techniques using this sample. The main goal of the present paper is to test the well-known dental calcification and eruption standards proposed by Ubelaker (1989). For that purpose, the maxilla, upper and lower, of each individual was X-rayed. Other methods tested are the maximum diaphyseal length and union of bony epiphyses. Each observation was done without the previous knowledge of individuals' age at death. The percentages of correct classification are given by maxilla and by sex. Cause of death was also investigated as a potential factor affecting the validity of the indicators under

analysis, mainly tooth emergence. The comparative analysis of the various methodologies was statistically analyzed. It is shown that tooth formation appears to be a more reliable indicator than tooth eruption and works much better than the other tested methodologies. Besides the asymmetry found in a same individual, the results clearly show that each method reaches its best performance in a given age interval.

Weidenreich revisited: morphology of the Upper Cave crania. DL CUNNINGHAM, University of Missouri, Columbia 65211

Upper Cave 101 and Upper Cave 103 are *Homo sapiens* fossils from Zhoukoudian, China that figure prominently into discussions of modern human origins. Adherents to the Multiregional model argue that these fossils exhibit characteristics found in modern Asian populations while proponents of the Out-of-Africa model observe no distinctive Asian features, and frequently point out African characteristics which were allegedly retained from the initial exodus of modern humans.

UC 101 and UC 103 were compared to Howells' modern human groups and Paleoindian and Archaic Indian crania using unweighted, unrestricted canonical variate analysis (CVA) and associated Mahalanobis Distance Analysis. Results indicate that it is unlikely that these two fossils represent the same population, contrary to interpretation based on archaeological context. IFUC 101 and UC 103 were from the same contemporaneous group, ancient East Asians exhibited more within-group morphological variation than do modern populations.

While UC 101 is classified as Easter Island in the distance analysis, its similarities to European, Eskimo, African, and Archaic Indian populations can be seen in the CVA plots. UC 103, on the other hand, is much more of an outlier to modern populations in the plots. Although the CVA allies this fossil most closely with Archaic Indians, the Lime Creek Paleoindian, and Easter Island, the distance analysis consistently classifies it as Australo-Melanesian. However, UC 103 has much lower typicality probabilities associated with the distance analyses than does UC 101.

No overriding support for either school of modern human origins is found. Results do indicate that 25,000 years ago, East Asia was inhabited by people morphologically similar to modern Polynesians and Australo-Melanesians, explaining why many of the first Americans tend to resemble modern South Pacific populations. This also attests to a short time depth for modern East Asian morphology.

The phylogenetic significance of new *Copelemur* material from early Eocene beds of the Washakie Basin, Wyoming. F.P. CUOZZO and H.H. COVERT, Anthropology, University of Colorado, Boulder, CO 80309-0233.

The Notharctinae experienced a broad and successful adaptive radiation in North America during the early and

middle Eocene. While known from an extensive and well studied fossil record, ongoing debate exists on the phylogenetic relationships among the six genera that make up this adapid subfamily. Here we describe new specimens of *Copelemur*, one of the least well known and most geographically restricted notharctine genera. This new material is of interest because *Copelemur* has been argued to represent an evolutionary dead end by some, to be the sister taxon of *Smilodectes* by Beard (1988), and to be the sister taxon of a group including both *Smilodectes* and *Notharctus* by Covert (1985, 1990).

The new material described here is from Lysitean beds of the Washakie Basin, southcentral Wyoming. Much of this material is provisionally assigned to the species *Copelemur australotutus*, as this material exhibits the diagnostic traits of this taxon as described by Beard (1988). These traits include more distal entoconids and less distinct entocristids when compared to *C. tutus*, and a size intermediate between *C. tutus* and *C. praetutus*. New specimens include several jaw fragments with more than one tooth and a right dentary preserving P3 through M3. This new material greatly increases the *C. australotutus* hypodigm, as well as the *Copelemur* hypodigm in general, and allows us to better understand the degree of morphologic variation within the genus than had been previously known. For example, traits previously used in the phylogenetic analysis of *Copelemur* such as the mesiodistal position of the molar entoconids and the location and size of the molar paraconids exhibit substantial variation in a sample from a single locality. Because these traits vary more than previously recognized, previous analyses of notharctine relationships must be reviewed in light of these new data. Moreover, both Beard's and Covert's phylogenetic hypotheses are slightly weakened. Finally, the molar shear crests of these new specimens support previous conclusions that *Copelemur* resembles both *Smilodectes* and *Notharctus* in being more folivorous than early Eocene notharctines. Thus, it is possible that habitus features are compounding this phylogenetic debate. We thank the Wyoming BLM for permission to work in the Washakie Basin.

The landscape distribution of larger mammal taxa in eastern Lowermost Bed II, Olduvai Gorge, Tanzania. A.E. CUSHING and R.J. BLUMENSCHINE, Dept. of Anthropology, Rutgers University, New Brunswick, NJ 08901.

We present the landscape distribution of larger mammal and aquatic taxa in the eastern part of Lowermost Bed II Olduvai Gorge which has been recovered by the Olduvai Landscape Paleoanthropology Project (OLAPP) from 1989-1997. We develop a new model describing the variation of the environment over space during the discrete time period of 1.7 mya at Olduvai. Although previous environmental reconstructions for this area have been proposed, none have benefited from a landscape-scale database. The 10 km² study area on the eastern margin of the paleo-lake contains a variety of browsers, grazers and larger aquatic animals. A groundwater wetland is a focal point on the landscape where a diversity of taxa including an equal number of open area-grazing genera and more closed area-browsing types were recovered. Preliminary results suggest that the numbers of browsing taxa drop and grazing taxa increase further east and further west of this

'core' wetland area. Aquatic animals such as fish, crocodile, and hippopotamus also diminish with distance from this central area. The farthest eastern and western (or lakeside) excavations reveal only grazing mammals. The groundwater wetland habitat, therefore, appears to hold browsers in a bushland or wooded bushland. No faunal specimens recovered represent a closed woodland. Several other lines of evidence, such as skeletal part profiles and bone condition as it pertains to weathering and breakage, support this scenario of a semi-closed bushed but not densely wooded groundwater wetland, surrounded by a slightly more open ecotone, and finally giving way to mostly open grasslands to the eastern and western limits of this sampling area.

Supported by the National Science Foundation and the Center for Human Evolutionary Studies at Rutgers.

Do genes for body weight also influence bone mineral density? S.A. CZERWINSKI, M.C. MAHANEY, J. BLANGERO, J. ROGERS, Department of Genetics, Southwest Foundation for Biomedical Research, San Antonio, TX.

Many studies have demonstrated a positive correlation between body weight and bone mineral density (BMD) in humans, with heavier people having greater bone mineral density. Many other factors also contribute to variation in bone mineral density. Among these are genetics, age, dietary intake and exercise. This study investigates the relationship between body weight and bone mineral density as measured in the appendicular (AP) spine in a sample of 673 baboons from 12 pedigrees housed at the Southwest Foundation for Biomedical Research. The animals range in age from 5.4 to 27.8 years. Weight is measured using a standardized anthropometric procedure. BMD is assessed using dual energy x-ray absorptiometry. Mean body weight for the sample is 22 kg (10-65 kg), while mean BMD is 1.24 g/cm² (0.88-2.09 g/cm²).

Bivariate variance components analysis using a maximum likelihood estimation procedure is used to estimate the total phenotypic, environmental and genetic correlation between body weight and bone mineral density while simultaneously controlling for other factors including age, sex, crown-rump length, sub-species admixture, and degree of osteophytosis in the spine. There are significant heritabilities (h^2) for both body weight ($h^2=0.34$, $p<0.001$) and AP spine BMD ($h^2=0.24$, $p<0.001$). The overall phenotypic correlation (ρ_P) between the two traits is 0.36. The genetic correlation (ρ_G) between body weight and BMD is 0.28 ($p=0.04$), while the environmental correlation (ρ_E) is 0.48 ($p<0.001$). Thus, genes that influence both body weight and AP spine BMD are responsible for ~8% of the additive genetic variance in AP spine BMD. Of greater influence however are common environmental factors which account for ~23% of the residual (i.e. non-genetic) phenotypic variation in both BMD and body weight in these non-human primates. These results show that the phenotypic relationship between body weight and BMD is

most strongly influenced by shared aspects of the physical environment such as diet or exercise that may influence both traits.

Supported in part by AXYS Pharmaceuticals, Inc.

Temporal trends in morbidity in the Chesapeake Bay area: Part One. Samples, methodology, and context. F.E. DAMANN, Louisiana State University, Baton Rouge, LA, 70803, E. MILLER, California State University, Los Angeles, CA, 90032, E.B. JONES and D.H. UBELAKER, Department of Anthropology, National Museum of Natural History, Smithsonian Institution, Washington, DC, 20560.

The ecological zone of the Chesapeake Bay area provided favorable conditions for the development of many Woodland period Algonquian-speaking tribes. Today, the archaeological record indicates a proliferation of Native populations in the Chesapeake Bay area during the Early Woodland period until European settlement. Examination of skeletal indicators of morbidity in samples from this region facilitates better understanding of Native American cultural transitions throughout prehistory and European Contact. In this paper a regional overview, study methods, and research goals are discussed.

Human skeletal samples from nine archaeological sites found in the Chesapeake Bay region were studied to show temporal patterns of health in ancient populations. Sites chosen for review encompass nearly 1,700 years of Chesapeake Bay history, beginning with the Early Woodland period (BC 1000) and extending to Contact (AD 1630). Combining all nine sites yielded nearly 700 individuals. Previous research in temporal health trends suggested a mean decrease in community health with the origin of agriculture, increased population size, and European arrival. With this in mind, we recorded nonspecific health indicators such as porotic hyperostosis, cribra orbitalia, caries, abscessing, enamel hypoplasia, antemortem tooth loss, forearm trauma, periosteal reaction, and spondylolysis. These indicators were chosen because of their significance to understanding stress patterns within populations. Results of this study are discussed in the associated paper "Temporal trends in morbidity in the Chesapeake Bay area: Part Two. Data and conclusions."

Status and Health among the Ancient Maya at Tikal, Guatemala. M.E. DANFORTH, Department of Anthropology and Sociology, University of Southern Mississippi, Hattiesburg, MS 39406-5074.

In societies with ascribed status, differential access to resources affects juveniles as well as adults, which in turn may be reflected in patterns of childhood health disruptions. Such patterns were investigated at Tikal, Guatemala. As one of the largest Maya centers, it offers

a clearly stratified population that underwent extensive culture change from AD 300 to 900.

Fifty mandibular canines, dating from the Preclassic to the Late/Terminal Classic, were evaluated. The sample was composed predominantly of adult males, but the four social strata (elite, servant/elite, middle, and lower) were fairly evenly represented. Thin sections were scored for three enamel microdefects: striae of Retzius, Wilson bands, and linear enamel hypoplasias. Frequencies of defects as well as ages-at-formation were considered.

Results show the Early Classic subpopulation to display higher levels of both striae and Wilson bands compared to Late Classic individuals, but lower frequencies of hypoplasias at all ages. When differences by social status are considered in the combined intertemporal sample, the lower classes not only have more striae, but exhibit more than twice the level of hypoplasia formation seen among elites, again this pattern being present throughout childhood. When differences by status within time periods are considered, patterns become more varied since sample sizes are markedly reduced. Within the Late Classic subpopulation, however, upper class individuals consistently display lower frequencies of striae and hypoplasias.

These findings suggest that lower class juveniles experienced increased levels of health disruptions compared to their middle class and elite counterparts throughout the Classic period. They also provide tentative support for other studies (eg, Haviland 1967) concluding that conditions, particularly those resulting in longer term stress, may have worsened over time at Tikal. These patterns are compared with those seen at other Maya sites.

Inadequacies of the intermembral index in platyrrhines. L.C. DAVIS and S.M. FORD, Dept. of Anthropology, Southern Illinois University, Carbondale, IL 62901-4502.

The intermembral index (IMI) is widely held as both a strong indicator of locomotor habit and a correlate of body mass in primates. As such, it is frequently employed in reconstructions of fossil taxa. This study examines the nature of the relationship between IMI and body mass, locomotion, and relative limb length across platyrrhine primates.

Data collected by both authors on limb segment lengths in 48 platyrrhine species were supplemented by data from Dykyj (1983). Body mass and locomotor data were taken from the literature. The relationship between IMI, body mass, and behavior has been most extensively studied in prosimian and catarrhine primates. While Dykyj's (1983) study examined these relationships in platyrrhines, she was limited to using Erikson's gross behavioral categories, and body mass data were rare. The present study uses the significantly more extensive and detailed positional behavior and body mass data currently available, and incorporates more platyrrhine species.

Previous studies have demonstrated a significant 'trend' towards increasing IMI with increasing body mass in both prosimians and catarrhines. In our platyrrhine sample, however, this correlation is weak ($r^2=0.68$), and the slope of this regression is nearly flat (slope=0.09). This relationship disappears, or is even reversed, when

looking at smaller taxonomic groups (families, subfamilies, genera) or when the atelines are removed from the sample. Thus, the IMI/body mass relationship reported in other primates is not found in platyrrhines.

Among prosimians and catarrhines, IMI has been shown to correlate with locomotor mode. However, among platyrrhines for which there are data, there are no significant correlations between IMI and frequencies of leaping, quadrupedalism, or climbing. In addition, several platyrrhine species pairs with identical IMI exhibit widely different fore- and hindlimb lengths relative to body mass. This seriously confounds any attempt to accurately predict locomotor mode from IMI alone.

Our analysis demonstrates the absence of a strong or predictable relationship between IMI and body mass, locomotor mode, and relative limb length in platyrrhine species. Several explanations are explored. In addition, we urge that IMI be used with extreme caution when reconstructing behavior in fossil platyrrhines.

Research supported by NSF (DBS 9203884), Sigma Xi, the Andrew Mellon Foundation, and the Smithsonian Institution.

The crucial role of scaling methods in comparative tests of primate cognitive evolution. R.O. DEANER, Department of Biological Anthropology & Anatomy, Duke University, Durham NC 27708

The social strategizing hypothesis posits that the need to manipulate the social environment has selected for primate cognition. In contrast, the ecological hypotheses of spatial mapping and extractive foraging emphasize the selective impacts of locating and manually processing foods, respectively. Although early comparative anatomical studies supported the ecological hypotheses, more recent work has favored the social strategizing hypothesis. One difference between early and later studies is that early studies scaled cognitive structures (a) by comparing them to interspecific regressions of the structure in question on body mass, while later studies scaled cognitive structures (b) by comparing them to interspecific regressions of the structure in question on the rest of the brain or (c) by taking a ratio of the structure in question over the rest of the brain. Here I review these three methods and show that they all make untested assumptions.

To explore the practical significance of using different scaling methods, I performed a series of comparative tests. Specifically, I examined the ability of a social variable, group size, and an ecological variable, home range size, to explain variation in the anthropoid non-visual cortex (NVC) when the NVC was scaled with the three different methods. In multiple regression with independent contrasts, home range size was a better predictor of NVC variation than group size when scaling method (a) was used but group size was a better predictor when methods (b) and (c) were employed.

This study indicates that workers should focus increased attention on developing valid scaling methods and should reserve judgment as to whether ecological or social forces are more important in the evolution of primate cognition.

Depressive symptoms, unemployment, and father-absence: A preliminary comparison of rural and urban Batswana men. S.A. DECKER, Anthropology, Emory U, Atlanta, GA 30322; sdecker@emory.edu

Depression is one of the fastest growing causes of morbidity and mortality, particularly in developing nations which have been the traditional research domain of biological anthropologists. As a psychobiological illness with a complex social and biological etiology, depression may be understood more fully with a cross-cultural, biocultural perspective. Preliminary analyses assess the association of four common risk factors with level of depressive symptoms (LDS): rural compared to urban residence; absence of father during childhood; perceived frequency of social stressors; and unemployment or economic dependency. Further analyses will include repeated measures of salivary cortisol.

Data were gathered during eight-months of ethnographic fieldwork in a remote rural village (~500 Pop) and a large city (~150,000 Pop) in Botswana. Participant observation, and informal interviews provided a qualitative information base throughout the study. Two interviews of between one- and two-hours were conducted with 28 rural men, and 29 urban men between the ages of 20-years and 58-years. The Beck Depression Inventory was used to assess level of depressive symptoms (LDS). An abbreviated version of the Pearlin and Schooler chronic stressor inventory was used to assess perceived frequency of social stressors. Other data include basic demographic data, life-histories, and retrospective Lickert-ratings of childhood happiness.

The best-fitting regression model was determined using a backwards stepwise multiple-variable linear regression algorithm in SYSTAT with a 0.05 significance level for removal and re-entry. Partial regression results indicate that LDS associates positively and separately with the following four factors: residence in the rural village ($F=5.86$, $P=0.02$, $R^2=0.113$); father-absence prior to age 13-years ($F=4.53$, $P=0.04$, $R^2=0.087$); perceptions of more frequent social stressors ($F=4.79$, $P=0.03$, $R^2=0.092$); and unemployment or economic-dependency ($F=9.05$, $P=0.001$, $R^2=0.174$). Overall the model is highly statistically significant ($P(F>24.239)$ with $F_{4,52}=0.001$, with an $R^2=0.435$). Age, educational attainment, gross yearly income, and marital status do not associate with LDS.

Supported by a grant from the National Science Foundation, Physical Anthropology.

The Hypoglossal Canal: Making Silent Skulls Speak? D. DEGUSTA, W. H. GILBERT, Dept. of Integrative Biology, and S. P. TURNER, Dept. of Anthropology, University of California, Berkeley, CA 94720-3140.

The mammalian hypoglossal canal transmits the nerve that supplies the

muscles of the tongue. The size of the hypoglossal canal has been used to date the origin of human-like speech capabilities to at least 400,000 years ago and to assign modern human vocal abilities to Neanderthals (Kay et al., 1998, PNAS 95:5417). These conclusions are based on two hypotheses: 1) the size of the hypoglossal nerve is correlated with the size of the hypoglossal canal, and 2) the size of the hypoglossal canal is correlated with speech abilities.

We tested the first hypothesis by examining the relationship between hypoglossal canal and nerve size in a sample of human cadavers. We found no apparent correlation between nerve size and canal size.

We tested the second hypothesis by examining the size of the hypoglossal canal in 75 non-human primates and 104 modern humans. A number of non-human primate specimens have hypoglossal canals that are within the size range of our human sample, both absolutely and after correction for oral cavity size. We also examined the size of the hypoglossal canal in several fossil hominid specimens and found additional taxa with modern human-sized canals.

Our results demonstrate that the size of the hypoglossal canal is not a reliable indicator of speech. The timing of the origin of human language and the speech capabilities of Neanderthals thus remain open questions.

Expanded alleles and hypermutability at a trinucleotide repeat locus in the general population: implications on the stability of the human genome. R. DEKA, S. GUANGYUN, D. SMELSER, S. CHUNHUA, Department of Environmental Health, University of Cincinnati, Cincinnati, OH 45267, and R. CHAKRABORTY, Human Genetics Center, University of Texas School of Public Health, Houston, TX 77225.

Over a dozen human hereditary diseases have been shown to be caused by expansions of trinucleotide repeats. All of these repeat loci are, however, normally polymorphic in human populations. Disease results when the repeat arrays become longer than a certain threshold. In the case of CAG repeat associated diseases, the longest normal allele does not exceed 40 repeats. A recent report (Nature Genet 17: 385-386, 1997) describes a polymorphic CAG repeat locus (ERDA1 located on chromosome 17q21) with alleles as large as 50-90 repeats without any disease association. We have analyzed this locus in four human populations (German, Nigerian, Chinese and New Guinea Highlander). Two distinct classes of alleles defined by the length of the CAG repeat units are observed: (1) shorter alleles of size 10 to 40 repeats and (2) longer alleles of size 53 to 90 repeats. No intermediate size alleles between these two classes are observed. Although there is significant inter-population variation in the distribution of alleles, the most notable

observation is the prevalence of the longer alleles among the New Guineans (27%) and rarity of these alleles among the Nigerians (5%). The frequency among the Germans and the Chinese is 17% and 24%, respectively. Next to assess the inter-generational stability of the alleles, we examined 725 meioses. A total of 46 mutations were detected, all of which remarkably arose from alleles larger than 50 repeats. This gives a mutation rate of 6.3%, which albeit is an underestimate given the mutations are exclusively confined to the larger repeats. At least 67% of the mutations are contractions. These observations raise new questions on the stability of the human genome. Expansion and instability at triplet repeats are features of disease causing loci. ERDA1 has not yet been shown to be associated with any known disease, and if holds out to be true, we are yet to appreciate the dynamics of the "normal" genome.

Supported by NSF grant SBR 9600910 and NIH grants GM 45861, 53545 and 41399.

Effects of neurocranial surgery on basicranial growth in isolated sagittal synostosis. V.B. DELEON, M.P. ZUMPAÑO, J.T. RICHTSMIEIER, Johns Hopkins University School of Medicine, Baltimore, MD 21205.

Isolated sagittal craniosynostosis produces a distinctive scaphocephalic neurocranium that has been described extensively in the literature. Abnormal basicranial morphology in this form of synostosis has also been noted, providing further evidence of the interrelated growth patterns of the neurocranium and basicranium. Surgical correction of cranial morphology ranges from simple strip craniectomies to more elaborate bone-flap procedures, but in almost all cases the immediate impact of the surgical procedure is restricted to the neurocranium. This study addresses the secondary effects of neurocranial surgery on the cranial base.

We obtained 3-D CT scans for three groups: a young (0-1 year old) pre-operative group (N=16), an older (1-2 years old) pre-operative group (N=3), and an older (1-2 years old) post-operative group (N=9). Landmark data from bregma, lambda, and eleven points on and around the cranial base were collected from 3-D CT reconstructions and analyzed using Euclidean Distance Matrix Analysis (EDMA). Form differences between the young and older pre-operative groups were considered to represent growth under the influence of a fused sagittal suture. Form differences between the young pre-operative and older post-operative groups were considered to represent a combination of immediate surgical alteration and growth under the influence of a surgically modified suture system.

We found three notable trends in the growth of unoperated sagittal synostosis patients: i) very little increase in cranial height (represented by distances from bregma to points on the cranial base); ii) significant superoinferior thickening of the sphenoid body; and (iii) widening of the posterior cranial fossa. In children who underwent surgical intervention, we found greater relative distances from bregma to points on the cranial base, demonstrating that surgery permitted greater superoinferior expansion of the endocranial space. In addition, there was no post-operative increase in the thickness of the sphenoid body and much less widening of the posterior cranial fossa.

These results demonstrate that surgical alteration of the fused neurocranium produces related changes in the morphology of the cranial base. However, because surgery cannot recreate a functional sagittal suture, it remains to be shown whether the basicranium is more similar morphologically to a normal basicranium, or whether it is distinct from both the normal and fused-suture morphologies.

This work was supported by NIDR grant 1 P50 DE11131-01 and a NSF graduate research fellowship.

Associations between birthweight and blood pressure in adulthood: The Fels Longitudinal Study. E.W. DEMERATH, B. TOWNE, W.C. CHUMLEA, and R.M. SIERVOGEL. Division of Human Biology, Wright State University School of Medicine, Dayton, OH 45435.

The "fetal origins hypothesis" (Barker et al., 1989, *British Medical Journal* 298:564-7) proposes that pre-natal growth (as measured by birthweight) is predictive of the risk of hypertension and other cardiovascular diseases in adulthood. However, these reports are from retrospective analyses of birth records. Given the numerous physiologic and behavioral processes that intervene between birth and the adult onset of hypertension, it is appropriate to examine this hypothesis using serially measured data.

In the present analysis, the relationship between birthweight and blood pressure was examined in 346 individuals (169 males and 177 females) born between 1929 and 1967 and followed from birth to adulthood (mean age 45 years; range 30-59 years) in the Fels Longitudinal Study. Subjects were grouped by birthweight ("low"= lowest quartile: mean weight 2.6 kg; "high"= highest quartile: mean weight 3.4 kg; and "average"= middle quartiles). Differences in means were tested using analysis of variance for uneven sample sizes. Models tested included current and past BMI as covariates.

The mean BMI at age 45 years was 26 kg/m² in both sexes. Systolic and diastolic blood pressures (TEM = 2 mm Hg) measured at age 45 years were 121/77 in males and 111/68 in females. Mean systolic blood pressure was approximately 6 mm higher in males having low birthweight than in the average birthweight group ($p < 0.05$). Systolic blood pressure was not associated with birthweight in females, and diastolic blood pressure was not related to birthweight in either sex.

While BMI in low birthweight males was not significantly different from BMI in average birthweight males during childhood and youth (ages 1, 2, 3, 6, 9, and 18 years), their BMI at age 45 years was significantly higher (27.4 kg/m² vs. 25.3 kg/m², $p < 0.005$). This was due to their greater increase in body weight from age 18 to age 45 years compared to average birthweight males (20 kg vs. 15 kg, $p < 0.001$). When BMI at age 45 was added to the model, birthweight was no longer associated with male systolic blood pressure. Neither BMI at age 45 years nor change in weight from age 18 to 45 years was related to birthweight in females.

This study indicates that low birthweight in males is associated with higher systolic blood pressure at age 45. However, this relationship is likely due to the development of higher BMI in low birthweight males after age 18 years.

Supported by NIH grants HD12252, HD31621 and American Heart Association Post-doctoral Fellowship #98-04582.

Bone strain in the macaque tibia during functional activity. B. DEMES, Y. QIN, J.T. STERN, S.G. LARSON, and C.T. RUBIN, Depts. of Anatomical Sciences and Biomedical Engineering, SUNY at Stony Brook, NY 11794.

The functional loading environment of the macaque tibia was analysed using three 3-element rosette strain gauges applied to the bone around the circumference at midshaft. Strains were recorded during walking and galloping at a range of speeds. For 93 steps, principal strains, their angles to the long axis of the bone, and the normal strain distribution in the midshaft cross section were calculated.

During the stance phase, bending is the predominant loading regime of the tibia, accounting for more than

90% of total strains. The neutral axis of bending forms a small angle with the frontal plane for galloping steps, and a somewhat larger angle for walking steps, putting the lateral cortex into moderate compression (up to -400 μ strains), the medial into moderate tension (up to 400 μ strains). Midstance tensile strains at the anterior cortex are 1914 ± 573 μ strains, compressive strains at the posterior cortex -1968 ± 578 μ strains for gallops. The corresponding values for walking steps are 1096 ± 279 and -1150 ± 203 , respectively. The large standard deviations reflect a wide range of speeds.

Bone strains in the tibia are similar in magnitude to strains recorded for the ulna of the same animal at comparable speeds. This similarity occurs despite the fact that primates carry more weight on their hind limbs and these limbs also dominate propulsion. Bending was also found for the ulna, but this bone was bent medially concave by the ground reaction force that passes medially to the abducted limb. The hind limbs are not abducted during stance and experience anteroposterior bending instead. The tibial midshaft of macaques is shaped to offer greater bending strength anteroposteriorly. The fibula may help to channel bending into this plane. The slight laterally concave curvature of the tibia may be responsible for the minor side-to-side loading with the lateral surface in compression.

Supported by NSF SBR 9507078.

Variation in hominid brain size: How much is due to method? C. DE MIGUEL and M. HENNEBERG, Anatomical Sciences, University of Adelaide, Adelaide SA 5005, Australia

Brain size assessed by means of cranial capacity (CC), is one of the most frequently analysed metric characters of hominids. Accuracy of individual CC estimates depends on completeness of specimens and methods used for reconstruction and measurement. A file of all published estimates of CC of hominids dated from 3.3 Ma to 10 Ka including 406 estimates for 209 specimens was compiled. In the file, 47 specimens are available with 3 to 10 estimates obtained by various methods and/or by various authors. Sixteen of those specimens were dated at more than 1 Ma, and 31 at 1 Ma or less. Using individuals as classes in ANOVA, intraclass variation which represents "error" of estimates was calculated. For the total sample of multiple estimates ($N=193$) the "error" variance is 5296.8 ml^2 . This constitutes 21.5% of the total variance of CC in the modern *Homo sapiens*, and similarly large percentages of the variance in variously grouped fossil hominid species. The "error" standard deviation is 72.8 ml which amounts to a coefficient of variation (CV) of 7.0, quite large in comparison to the total CV in modern humans (11.6). The "error" variances for the older (over 1 Ma) and more recent specimens are similar when expressed as CVs - 8.0 and 6.7 respectively. This corresponds to the average

range of estimates for the same specimen from 50 ml to 100 ml depending on its CC.

In actual repeated ten times measurements of Stw 505 (research quality cast), we obtained estimates ranging from 474 ml to 574 ml depending on the method (water, mustard seed, plasticine, midline determination) and observer.

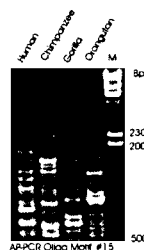
Sizeable "error" variance of individual hominid CC estimates makes us wonder whether any specimen can be reliably placed on one or the other side of a particular "cerebral Rubicon" between palaeospecies.

Supported by the Wood Jones Bequest and the University of Adelaide.

Use of arbitrary-primed PCR (AP-PCR) oligonucleotide motifs for genomic and phylogenetic analyses of human and non-human primates. E.J. DEVOR, Integrated DNA Technologies, Coralville, IA 52241

Molecular studies of the genomes of both human and non-human primates are benefiting from an ever-increasing number of new molecular tools and types of analyses. The technique of arbitrary primed-PCR (AP-PCR) is one such tool. Following Williams et al. (Nucleic Acids Res., 18: 6531-6535), AP-PCR produces stable, reproducible amplicons from genomic DNAs using a single random oligonucleotide primer sequence of 10 - 12 bases under low stringency conditions.

Here, twelve different AP-PCR primer motifs are used to generate amplicons ranging in size from 200bp to 2Kbp using both human and non-human primate DNAs (see Fig. for example of an AP-PCR gel).



It will be shown that these amplified random fragments are stable, reproducible, and polymorphic. A simple means of isolating and cloning individual AP-PCR fragments for more detailed study will also be demonstrated.

The primary advantage of using AP-PCR as an adjunct to other methods of genomic analysis is that the amplicons generated from the primer motifs are random and, therefore, useful for both within and between genome studies. Also advantageous is that the primers are short and, consequently, inexpensive. Moreover, they are used singly rather than in pairs as in traditional PCR amplifications.